

GenCore version 4.5  
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On nucleic - nucleic search, using sw model

Run on August 31, 2002, 20:00:14 Search time 413.21 seconds  
(without alignments)  
6664 986 Million cell updates/sec

File: US-09-678-303-1

Perfect score: 1350  
Sequence: 1 cgaagcggccggcgtgtgtata..... gatgtgtccatgagatcttcc 1350

Scoring table:

IDENTITY\_NTC

Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10453268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Genbank:  
1: gb-ba.\*  
2: gb-ba.\*  
3: gb-in.\*  
4: gb-in.\*  
5: gb-ov.\*  
6: gb-pat.\*  
7: gb-pat.\*  
8: gb-pat.\*  
9: gb-pat.\*  
10: gb-pat.\*  
11: gb-sis.\*  
12: gb-sys.\*  
13: gb-un.\*  
14: gb-vi.\*  
15: em-ba.\*  
16: em-ba.\*  
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32: em-ba.\*  
33: em-ba.\*

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No. Query Match length DB ID Description

1	1350	100.0	1350	6	AX105267	AX105267 Sequence
2	971	71.9	971	6	AX105268	AX105268 Sequence
3	731	54.1	731	6	AX105269	AX105269 Sequence
4	458.4	34.0	1505	6	PSPLNS	PSPLNS
5	191.8	14.2	623	6	AX036596	AX036596 Sequence
6	191.8	14.2	834	6	AX036595	AX036595 Sequence
7	189.6	14.0	326	6	AX036597	AX036597 Sequence
8	181.2	13.4	653	6	AX036598	AX036598 Sequence
9	180.6	13.4	998	6	PSPEPT	PSPEPT
10	170	12.6	721	6	ENPCAMP	ENPCAMP
11	161.8	12.0	510	6	LEPLACY	LEPLACY
12	152.8	11.3	504	6	AF334384	AF334384
13	152.8	11.3	541	6	AF334385	AF334385
14	152.8	11.3	705	6	AF334386	AF334386
15	152.8	11.3	724	6	AF334387	AF334387
16	152.8	11.3	724	6	AF334388	AF334388
17	152.8	11.3	740	6	AF334389	AF334389
18	152.8	11.3	53889	6	AX031546	AX031546
19	142.8	10.6	605	6	AX031546	AX031546
20	142.8	10.6	605	6	AX031546	AX031546
21	142.8	10.6	605	6	AX031546	AX031546
22	128.2	9.5	1716	6	ALPHYT	ALPHYT
23	128.2	9.5	1716	6	MS018206	MS018206
24	116	8.4	207	6	AY036598	AY036598
25	113.2	8.4	773	6	SPPCYA	SPPCYA
26	111	8.2	720	6	AF031545	AF031545
27	107.6	8.0	69590	6	AC087771	AC087771
28	106.4	7.9	250	6	AX036600	AX036600
29	99.2	7.3	1447	6	ATHPG	ATHPG
30	99.2	7.3	15202	6	ATHPG	ATHPG
31	97.4	7.1	97554	6	AC009978	AC009978
32	95.2	6.9	676	6	AX036601	AX036601
33	95.2	6.9	155150	6	AX036602	AX036602
34	92.8	6.5	745	6	AF069412	AF069412
35	85.4	5.6	241	6	AX036599	AX036599
36	89	6.2	283	6	AX036603	AX036603
37	89	6.2	296	6	AX036604	AX036604
38	89	6.2	303	6	AX036605	AX036605
39	88.4	6.0	220	6	AX036606	AX036606
40	85.8	5.4	2242	6	PEAVAR3A	PEAVAR3A
41	84.2	5.2	67970	6	PEAVAR3A	PEAVAR3A
42	81	4.2	15194	6	AF135201	AF135201
43	81.8	4.1	170141	6	AF135201	AF135201
44	81.2	4.0	170141	6	AF135201	AF135201
45	80.8	6.0	90487	6	AL592166	AL592166

## ALIGNMENTS

RESULT 1	AX105267	1350 bp	INA	Linear	PAT 30 APR-2001
LOCUS	AX105267				
DEFINITION	Sequence 1 from Patent WO0125455.				
ACCESSION	AX105267				
VERSION	AX105267.1	GI:13921417			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS	Vezina, L.P. and D'Aoust, M.A.				
TITLE	Promoter for regulating expression of foreign genes				
JOURNAL	Patent: WO 0125455-A1 12-APR-2001;				
FEATURES					
source					

FASTA source  
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/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Sequence to be used as a promoter for regulating expression"  
expression" 216 3 230 3 402 1  
HASH COUNT 402 3 230 3 402 1  
ORIGIN









[illegible]

RESULT	9	998 bp	DNA	1000	1000	1000
LENGTH						
DEFINITION	Partial cDNA clone for plastocyanin.					
ACCESSION	X08434					
VERSION	X08434.1	01/2004				
KEYWORDS	chloroplast; coper; protective electron transfer; plastocyanin; thylakoid; thylakoid.					
SOURCE	Eucalyptus					
ORGANISM	Eucalyptus					
REFERENCE	Eukaryotic Vit. B12-plant-protein synthesis: Eucalyptus. Thylakoid A. Spectral properties of plastocyanin and its role in electron transfer from photosystem II to photosystem I. J. Biol. Chem. 267:10000-10004 (1992).					
AUTHORS	1 (bases 1 to 998)					
TITLE	Gray, J.					
JOURNAL	Direct Submission					
REFERENCE	Submitted (09 SEP 1992) J. Gray, University of Cambridge, Cambridge, UK					
TITLE	Plant Sciences, London Street, Cambridge CB2 3QA, UK					
KEYWORDS	2 (bases 1 to 998)					
REFERENCE	Gray, J. H. and Gray, J. C.					
TITLE	The first plastocyanin promoter directs cell specific but not cell type specific expression in transgenic tobacco plants					
KEYWORDS	Plant J. 3 (4): 457-449 (1993)					
REFERENCE	90030149					
COMMENT	A1-1 is a plant nuclear protein binding to the sequence AATATTAT in the promoters of light regulated genes (N. J. Gray & A. R. Cashmore). Binding of a pea nuclear protein to promoters of certain photoregulated genes is modulated by phosphorylation. The plant cell 11, 1069-1077, (1980).					
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SOURCE	1..998					
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	/cfeature="protein"					
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	208..224					
	repeat_region					
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	317..332					
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	333..351					
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	353..360					
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	401..417					
	misc_feature					
	418..435					
	misc_feature					
	436..453					
	misc_feature					
	454..471					
	misc_feature					
	472..489					
	misc_feature					
	490..507					
	misc_feature					
	508..525					
	misc_feature					



Asteridae: eumetazoids 1: Solanaceae: Solanum: Lycopersicon.

REFERENCE 1 (bases 1 to 51)

AUTHORS

DeLorenz, J.

TITLE

Direct Submission

JOURNAL

Submitted (02 JAN 1989) DeLorenz, J., University of Michigan, Chemistry Department, Ann Arbor, MI 48109, USA

REFERENCE 2 (bases 1 to 51)

AUTHORS

DeLorenz, J., DeLorenz, J., and DeLorenz, J., University of Michigan, Chemistry Department, Ann Arbor, MI 48109, USA

TITLE

Protein structure from X-ray crystallography

JOURNAL

Nucleic Acids Res 17 (15): 6414 (1989)

FEATURES

Source: local copy of protein

TRANSIT

peptide 1-192

CDs

1-192

old sequence

1-192

old sequence

1-192

old sequence

1-192

old sequence

1-192

old sequence

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old sequence

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old sequence

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old sequence

1-192

RESULT 12

AF344884

LOCUS

AF344884 504 bp mRNA linear 17 JAN 2001

DEFINITION

Arabidopsis thaliana putative RNA damage repair/oxidation protein (F14010.6) mRNA, complete cds.

ACCESSION

AF344884

VERSION

AF344884.1 GI:12247994

KEYWORDS

FLI CUNA

SOURCE

Thale cress.

ORGANISM

Arabidopsis thaliana

REFERENCE

Arabidopsis thaliana and Streptococcus mutans: a model for the study of oxidative DNA damage and its repair. In: Molecular Biology of the Cell, 11th Edition, W. H. Burgess, Jr., and W. H. Burgess, Jr., Eds., Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press, 1998, pp. 1-10.

AUTHORS

Yamada, K., Ito, S., Sakano, H., Pham, P. K., Bartholomew, J., and Goldsmith, A. D., Lee, J. M., Toriumi, M., Yano, K., Brooks, S., Chao, Q., Chen, H., Karlin, N., Nishimura, K., Kim, C., Lam, B., Miranda, M., Nishimura, K., Pham, P. K., Shinn, P., Southwick, A., Iwata, R. W., Pokor, J. R., and Theologis, A.

TITLE

Full length cDNA of gene F14010.6 (F14010.6)

JOURNAL

Submitted (09 JAN 2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

AUTHORS

Yamada, K., Ito, S., Sakano, H., Pham, P. K., Bartholomew, J., and Goldsmith, A. D., Lee, J. M., Toriumi, M., Yano, K., Brooks, S., Chao, Q., Chen, H., Karlin, N., Nishimura, K., Kim, C., Lam, B., Miranda, M., Nishimura, K., Pham, P. K., Shinn, P., Southwick, A., Iwata, R. W., Pokor, J. R., and Theologis, A.

TITLE

Direct Submission

JOURNAL

Submitted (09 JAN 2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

FEATURES

Source: local copy of cDNA

TRANSIT

peptide 1-192

CDs

1-192

old sequence

1-192

old sequence

1-192

old sequence

1-192

old sequence

1-192

old sequence

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old sequence

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old sequence

1-192

old sequence

1-192

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OY	1217	gctlltgtccaacaactlccacagtcgaacgcctgagagacaccattacatltaagaaccaal	1276
Dd	241	GCTTTATGCCAACAGCAGTTCCTCATFACGCTAAAGCAGAGAAGACATGTGTTCAAGANCAAC	300
OY	1277	gcttgatttctccaaacglttatcltcgatgaagacgcagatctcaagcgaggatlgatgct	1336
Dd	301	GTTATATACCCAAACAAATGTTATCTTGCATATGAATGAAATATCCAAAGTAGCTGAGGCTGG	360
OY	1337	gccaa	1340
Dd	361	GCCTA	364
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AFH271355			
LOCUS	Arabidopsis thaliana chloroplast partial K3P10TP gene for putative	541 bp	DNA linear P N 29 MAR 2001
DEFINITION	plasticocyanin.		
ACCESSION	AJ271355		
VERSION	AJ271355.1	GI:6723443	
KEYWORDS	K3P10TP gene; plastocyanin.		
SOURCE	thale cress.		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis		
REFERENCE	1 (bases 1 to 541)		
AUTHORS	Kieselbach,T., Hystedt,M., Hynds,P., Robinson,C. and Schroder,W.P.		
TITLE	A peroxidase homologue and novel plastocyanin located by proteomics to the Arabidopsis chloroplast thylakoid lumen		
JOURNAL	FEMS Lett. 480 (2-3), 271-276 (2000)		
COMMENT	20487156		
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		/gene="K3P10TP"	
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		/codon_start=1	
		/transl_table=1	
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		/protein_id="CA666894.1"	
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		YPHWVFDFDEIPIPGGVPAKISMDIEDILLNGCFEVALTEPTSYFCAPHQGADQM	
		VGRKIQM"	
		34..536	
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BASE COUNT	146 a	133 c	130 g
ORIGIN			127 t
Query Match	11.3%	Score 152.8,	DB 8, Length 541,

[illegible]

[illegible][illegible]

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QY 1097 tglgtcagaagcttccctceaaagacilltgaaglttgctgtgttgcacatgcttgcgaatgca 1156
DB 174 ACAGTCAACTCATCTCTTAAGAACTTGGAGTCGGCGGTAGCGGTGCACCTTCAATT 233
QY 1157 ttgttagctagaatgccccttgcagltgaagtgttgcgttagtgcagtgaggggtttg 1216
DB 234 GCTTTGGCCGGAAAGCCCATGGCAATAGAAATTCCTTGGAGAGAGAGATGGGATGGTA 293
QY 1217 gctttgttcccaaatlttcacagtgaacgcttgagagacaccattacattcaagaacaat 1276
DB 294 GCTTTTATTCCCAACGACTTCTCTATAGCTAAAGGAGAGAGATTGTCTTCAAGAACAAAC 353
QY 1277 gcttgcgttttccctcacaagcttacttgcagtgagaagaagaaatcccaagtgaggtt 1336
DB 354 GCTTGATACCAACAACTTGTGCTTCGATGAAGAGACATCCCAAGTGGCTTCGACGTG 413
QY 1337 gcaa 1340
DB 414 GCCA 417

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Search completed: September 1, 2002, 00:54:34  
 Job time: 17660 sec

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text outlines various methods for organizing and storing data, including digital databases and physical filing systems. It also mentions the need for regular audits and reviews to ensure the integrity of the information.

2. The second section focuses on the role of communication in achieving organizational goals. It highlights the importance of clear and concise communication, both internally and externally. The text provides examples of effective communication strategies, such as regular team meetings, open-door policies, and the use of various communication channels like email, phone, and face-to-face interactions. It also discusses the importance of listening and understanding the needs and concerns of all stakeholders.

3. The third part of the document addresses the challenges of managing a large and diverse workforce. It discusses the importance of providing ongoing training and development opportunities to keep employees up-to-date with the latest skills and knowledge. The text also touches on the importance of fostering a positive work environment and promoting a sense of team spirit and collaboration. It mentions the need for effective conflict resolution strategies and the importance of recognizing and rewarding employee achievements.

4. The final section discusses the importance of staying up-to-date with the latest trends and technologies in the industry. It emphasizes that continuous learning and innovation are key to long-term success. The text provides examples of how organizations can stay ahead of the curve by investing in research and development, attending industry conferences, and collaborating with external experts. It also mentions the importance of being flexible and adaptable to change.



550 Superficial: 1450 m<sup>2</sup>, 40% A, 20% V, 2400 g, 40% C, 20% other.

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Matches 150; Conflicts 0; Mismatches 0; Index 0; Gaps 0
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[illegible][illegible]

CC useful for regulating the expression of foreign genes in transgenic  
 CC organisms, particularly plants, e.g. monocotyledons, dicotyledons or  
 CC gymnosperms, by preparing a transgenic organism using an expression  
 CC construct comprising the promoter and an open reading frame (ORF) of a  
 CC gene.

XX Sequence 971 BP: 390 A; 141 C; 145 G; 295 T; 0 other;

Query Match 71.9%; Score 971; DB 22; Length 971;

Best Local Similarity 100.0%; Pred. No. 1,6e-182;

Matches 971; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 cgggtgtgtatattatgtgttcaataactcaaaacataaatttaagtacga 68  
 DB 1 cgggtgtgtatattatgtgttcaataactcaaaacataaatttaagtacga 60  
 QY 69 agtgcgtacattttctttgacaaaatattcaccctactctgttataatcatttga 128  
 DB 61 agtgcgtacattttctttgacaaaatattcaccctactctgttataatcatttga 120  
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 DB 121 aacatlaaqaataaaalagatgataaagaacaaagttagtattttgacacaaat 180  
 QY 189 ttgtgtcacacatttgacaaaattttgtgtctctcttccatgtgtcaaaaacatag 248  
 DB 181 ttgtgtcacacatttgacaaaattttgtgtctctcttccatgtgtcaaaaacatag 240  
 QY 249 agagagaaaagaagagagagagagagagagagagagagagagagagagagagag 308  
 DB 241 agagagaaaagaagagagagagagagagagagagagagagagagagagagagag 300  
 QY 309 caaaagtgtagcaaaaagatgtacaaatcatttgaggaatttgacaaaacacaca 368  
 DB 301 caaaagtgtagcaaaaagatgtacaaatcatttgaggaatttgacaaaacacaca 360  
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 DB 421 gaattttggaagtcataaaaagaagaataatttttaaatataaagaattgagt 480  
 QY 489 catttgatlaaacatgtagatatttaagaattgataaagatgtagatlaaagttgat 548  
 DB 481 catttgatlaaacatgtagatatttaagaattgataaagatgtagatlaaagttgat 540  
 QY 549 tagtaattagaatttgcgtcaaatttaattgacatttgacttccatataattgac 608  
 DB 541 tagtaattagaatttgcgtcaaatttaattgacatttgacttccatataattgac 600  
 QY 609 ccataagatcatttaactcattttatatttcataagatcaataaagaataacggtat 668  
 DB 601 ccataagatcatttaactcattttatatttcataagatcaataaagaataacggtat 660  
 QY 669 attaatccctcaaaaataaaacggtatatttactaaaatactcaagccacgttagag 728  
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 QY 729 gataacatcaatccaaacatccaaacatccgtatagatgaacccgctttaagccac 788  
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 QY 789 gaactcgtgacacatctacattatcaatcaacacatttccacacatctgagccaca 848  
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 QY 849 caaaaacacatccacatcttatacccatctctataaaaaaacacacattttagatctac 908  
 DB 841 caaaaacacatccacatcttatacccatctctataaaaaaacacacattttagatctac 900

QY 309 atttgatccatctcaaacatcaaaagagagagagagagagagagagagagagag 968  
 DB 901 atttgatccatctcaaacatcaaaagagagagagagagagagagagagagagag 960

QY 969 gaagaagaata 979  
 DB 961 gaagaagaata 971

RESULT 3

AAS02128

ID AAS02128 standard; DNA: 731 BP.

XX

XX AAS02128;

AC 16-JUL-2001 (first entry)

DT

XX Promoter #3 for regulating expression of foreign genes

DE

XX Promoter; Transgenic Plant; monocotyledon; dicotyledon; gymnosperm; ds.

KW

XX Synthetic.

OS

XX WO200125455-A2.

PN

XX 12-APR-2001.

PD

XX 02-OCT-2000; 2000WO-CO01144.

FE

XX 04-OCT-1999; 99US-0157129.

FX

XX (MED1-) MEDICAGO INC.

PA

XX Vezina L. D'Amour M.

PI

XX WPI; 2001-26316/27.

UK

XX Novel promoter for regulating expression of foreign genes in transgenic

PT organisms, more specifically in a leaf specific manner in transgenic

PT plants -

PT

XX Claim 1; Page 9; 9pp; English.

FS

XX The sequence represents the coding sequence of promoter #3 for regulating

CC expression of foreign genes in transgenic organisms. The promoter is

CC useful for regulating the expression of foreign genes in transgenic

CC organisms, particularly plants, e.g. monocotyledons, dicotyledons or

CC gymnosperms, by preparing a transgenic organism using an expression

CC construct comprising the promoter and an open reading frame (ORF) of a

CC gene.

CC

XX

XX Sequence 731 BP: 299 A; 113 C; 109 G; 210 T; 0 other;

Query Match

Best Local Similarity 54.1%; Score 731; DB 22; Length 731;

Matches 731; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 aagaagaaaagaagagagagagagagagagagagagagagagagagagagagag 308  
 DB 1 agagagaaaagaagagagagagagagagagagagagagagagagagagagagag 300  
 QY 309 caaaagtttaccaaaatagtttatacaaatattgaagaaatttgacaaagttacaga 368  
 DB 61 caaaagtttaccaaaatagtttatacaaatattgaagaaatttgacaaagttacaga 360  
 QY 369 aataaggttaattcgttcaataaataagagtagacgacattagagagatgtccattga 428  
 DB 121 aataaggttaattcgttcaataaataagagtagacgacattagagagatgtccattga 420  
 QY 429 gaattttggaagtcataaaaagaagaataatttttaaatataaagaattgagt 488  
 DB 181 gaattttggaagtcataaaaagaagaataatttttaaatataaagaattgagt 480





[illegible]

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PR 24-SEP-1999; 990S-0155659;
PR 28-SEP-1999; 990S-0156458;
PR 29-SEP-1999; 990S-0156596;
PR 04-OCT-1999; 990S-0157117;
PR 05-OCT-1999; 990S-0157753;
PR 06-OCT-1999; 990S-0157865;
PR 07-OCT-1999; 990S-0158029;
PR 08-OCT-1999; 990S-0158232;
PR 12-OCT-1999; 990S-0158369;
PR 13-OCT-1999; 990S-0159293;
PR 13-OCT-1999; 990S-0159294;
PR 13-OCT-1999; 990S-0159295;
PR 14-OCT-1999; 990S-0159329;
PR 14-OCT-1999; 990S-0159330;
PR 14-OCT-1999; 990S-0159331;
PR 14-OCT-1999; 990S-0159637;
PR 14-OCT-1999; 990S-0159638;
PR 18-OCT-1999; 990S-0159584;
PR 21-OCT-1999; 990S-0160741;
PR 21-OCT-1999; 990S-0160767;
PR 21-OCT-1999; 990S-0160768;
PR 21-OCT-1999; 990S-0160770;
PR 21-OCT-1999; 990S-0160814;
PR 21-OCT-1999; 990S-0160815;
PR 22-OCT-1999; 990S-0160980;
PR 22-OCT-1999; 990S-0160981;
PR 22-OCT-1999; 990S-0160984;
PR 25-OCT-1999; 990S-0161404;
PR 25-OCT-1999; 990S-0161405;
PR 25-OCT-1999; 990S-0161406;
PR 26-OCT-1999; 990S-0161359;
PR 26-OCT-1999; 990S-0161360;
PR 26-OCT-1999; 990S-0161361;
PR 28-OCT-1999; 990S-0161920;
PR 28-OCT-1999; 990S-0161993;
PR 28-OCT-1999; 990S-0161993;
PR 28-OCT-1999; 990S-0162142;
PR 29-OCT-1999; 990S-0162142;

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Query Match 11 %; Score 152 R; DR 21; Length 686;
Best Local Similarity 61.7%; Pred No. 35; 21;
Matches 232; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

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QY 977 atggcaccgcttacttcacacacgcttgcctatccatcatcctacacgcttcaagctcaaac 1036
DB 54 atggcctcagctaacctcagccacgcttgcacatccatccttccacgcttcaaacgctca 113
QY 1037 gcaagcaagcttcaagctcaagcttcaagcttcaagcttcaagcttcaagcttcaagctt 1096
DB 114 accatcaaatcctcgcacacgcttcaagcttcaagcttcaagcttcaagcttcaagcttca 173
QY 1097 tctgtcagaagcttccctcaaacgcttcaagcttcaagcttcaagcttcaagcttcaagctt 1156
DB 174 acagtaaatcctcgcacacgcttcaagcttcaagcttcaagcttcaagcttcaagcttca 233
QY 1157 tctgtcagaagcttccctcaaacgcttcaagcttcaagcttcaagcttcaagcttcaagctt 1216
DB 234 gcttggccgcgaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagca 293
QY 1217 gcttggccgcgaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagca 1276
DB 294 gcttggccgcgaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagca 353
QY 1277 gcttggccgcgaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagca 1336
DB 354 gcttggccgcgaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagca 413
QY 1337 gcaa 1340
DB 414 gcaa 417

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RESULT 8  
AAC34364

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ID AAC34364 standard; DNA; 789 bp.
XX
AC AAC34364;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SP0 ID NO: 6385.
XX
KW Hybridisation assay, genetic mapping, gene expression control;
KW Protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
FD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 990S-0121825;
XX 05-MAR-1999; 990S-0123180;
XX 09-MAR-1999; 990S-0123548;
XX 23-MAR-1999; 990S-0125788;
XX 25-MAR-1999; 990S-0126254;
XX 29-MAR-1999; 990S-0126785;
XX 01-APR-1999; 990S-0127452;
XX 05-APR-1999; 990S-0127453;
XX 08-APR-1999; 990S-0128714;
XX 16-APR-1999; 990S-0129845;
XX 19-APR-1999; 990S-0130077;
XX 21-APR-1999; 990S-0130449;
XX 23-APR-1999; 990S-0130951;
XX 28-APR-1999; 990S-0131244;
XX 30-APR-1999; 990S-0132048;
XX 30-APR-1999; 990S-0132048;
XX 30-APR-1999; 990S-0132407;
XX 04-MAY-1999; 990S-0132484;
XX 05-MAY-1999; 990S-0132485;
XX 06-MAY-1999; 990S-0132486;
XX 06-MAY-1999; 990S-0132487;
XX 07-MAY-1999; 990S-0132883;
XX 11-MAY-1999; 990S-0134256;
XX 14-MAY-1999; 990S-0134218;
XX 14-MAY-1999; 990S-0134219;
XX 14-MAY-1999; 990S-0134221;
XX 18-MAY-1999; 990S-0134378;
XX 19-MAY-1999; 990S-0134768;
XX 19-MAY-1999; 990S-0134941;
XX 20-MAY-1999; 990S-0135124;
XX 21-MAY-1999; 990S-0135353;
XX 24-MAY-1999; 990S-0135629;
XX 25-MAY-1999; 990S-0136021;
XX 27-MAY-1999; 990S-0136392;
XX 28-MAY-1999; 990S-0136782;
XX 01-JUN-1999; 990S-0137222;
XX 03-JUN-1999; 990S-0137528;
XX 04-JUN-1999; 990S-0137502;
XX 07-JUN-1999; 990S-0137734;
XX 08-JUN-1999; 990S-0138074;
XX 10-JUN-1999; 990S-0138540;
XX 10-JUN-1999; 990S-0138847;
XX 14-JUN-1999; 990S-0139119;
XX 16-JUN-1999; 990S-0139452;
XX 16-JUN-1999; 990S-0139453;
XX 17-JUN-1999; 990S-0139492;
XX 18-JUN-1999; 990S-0139454;
XX 18-JUN-1999; 990S-0139455;
XX 18-JUN-1999; 990S-0139456;
XX 18-JUN-1999; 990S-0139457;
XX 18-JUN-1999; 990S-0139458;
XX 18-JUN-1999; 990S-0139459;
XX 18-JUN-1999; 990S-0139460;

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Db 299 gctttggccgaagacgcctgacatagaagtctcttggagagagggatgggtgtta 358  
 QY 1217 gctttgttcccaatcattctcagtgagcgtggagacacccatccttaagacat 1276  
 Db 359 gctttatcccaagacctctctatagctaaaggagaaagattgcttcaagaacac 418  
 QY 1277 gctggttcccaacattatctcagatgaagacgaatcccaagcgggttctgtct 1336  
 Db 419 gctggtatcccaacattgctctcagatgaagacgaatcccaagcgggttctgtct 478  
 QY 1337 gcaa 1340  
 Db 479 gccca 482  
 RESULT 9  
 AA333777  
 ID AA233777 standard; cDNA; 605 BP.  
 AC AA233777:  
 XX 09-DRC-1999 (first entry)  
 DT  
 XX Tobacco plant resistance-associated cDNA fragment 102.  
 DE  
 XX Tobacco; plant; resistance; tobacco mosaic virus; TMV; infection;  
 KM protection; plant protection agent; phytophagous fungi; nematode;  
 KM insect pest; pathogen resistance; transgenic plant; diagnosis; ss.  
 XX Nicotiana tabacum.  
 OS  
 XX DE19813048-A1.  
 PN 30-SEP-1999.  
 XX  
 PD 25-MAR-1998; 98DE-1013048.  
 XX  
 PF 25-MAR-1998; 98DE-1013048.  
 XX  
 PR 25-MAR-1998; 98DE-1013048.  
 XX  
 PA (FARB) HAYER AG.  
 XX  
 PI Schreier P, Garbers C, Langen G, Kiedrowski S;  
 XX  
 DR WPI; 1999-552163/47  
 XX  
 P1 Nucleic acids useful for identifying compounds capable of inducing  
 P1 pathogen resistance in plants  
 P1  
 P1  
 P1  
 P5 Claim 1a: 66; 130pp; German.  
 XX  
 CC This invention describes novel cDNA molecules corresponding to tobacco  
 CC (Nicotiana tabacum) genes that are expressed in response to tobacco  
 CC mosaic virus (TMV) infection. Regulatory regions that provide specific  
 CC expression of the nucleic acids in connection with induced resistance  
 CC can be used to identify compounds useful for plant protection by  
 CC transforming a cell with a recombinant DNA molecule containing a  
 CC selectable and/or detectable marker linked to the regulatory region,  
 CC culturing the cell in the presence of a test compound or sample, and  
 CC identifying a compound or sample that suppresses or activates and/or  
 CC enhances expression of the marker. Host cells containing the nucleic  
 CC acid, or polypeptides encoded by the nucleic acids, can be used to  
 CC identify compounds that inhibit or activate a polypeptide involved in  
 CC induced resistance, by contacting the cell or polypeptide with one or  
 CC more test compounds and identifying compound(s) that specifically  
 CC modulate the activity of the polypeptide. Plant protection agents can be  
 CC prepared by formulating the identified compounds in a form suitable for  
 CC their uptake and optionally metabolism in organisms, especially  
 CC plants, phytopathogenic fungi, nematodes or insect pests. The nucleic  
 CC acids or regulatory regions, or corresponding vectors, or the nucleic  
 CC polypeptides encoded by the nucleic acids, or compounds identified as  
 CC above, can be used to improve the pathogen resistance of plants or to  
 CC produce transgenic plants. The nucleic acids or regulatory regions, or  
 CC vectors, cells, plants or plant tissues containing them, or the

CC polypeptides and antibodies to the polypeptides, can be used to screen  
 CC for new plant protection agents or genes involved in induction of  
 CC resistance in plants. Vectors containing the nucleic acids, or the  
 CC regulatory regions or recombinant DNA molecule or vectors containing  
 CC them, or the compounds identified as above, or the polypeptides or  
 CC antibodies, can be used in diagnostic compositions. AA234676-23888  
 CC represent fragments of tobacco cDNA which are associated with plant  
 CC resistance.  
 CC  
 XX  
 SO Sequence 605 BP; 169 A; 105 C; 137 G; 194 T; 0 other.  
 Query Match 10.6%; Score 142.8; DB 20; Length 605;  
 Best local similarity 71.1%; Pred. No. 3.2e-19;  
 Matches 189; Conservative 0; Mismatches 77; Indels 0; Gaps 0;  
 QY 1075 aacttccaatgccaaggcttctgtcagagctccctcaagaacttgagttgttc 1144  
 Db 3 aacctcaacaatcccaaatgagtaagaaagccttcaaaaatgagttgttc 62  
 QY 1135 tgttgcagctgtcgaatgagttgagttgagcaatgtccttgcagttgagttgttc 1194  
 Db 63 tgttgcagctgtcgaatgagttgagttgagcaatgtccttgcagttgagttgttc 122  
 QY 1195 tggagctagatgaggggttggcttggatcccaacatctcagatgaagcgttga 1254  
 Db 123 tggagctagatgaggggttggcttggatcccaacatctcagatgaagcgttga 182  
 QY 1255 caccattacatcgaagcaatgctgttctcctcgaacgttatcttctgaagaaga 1314  
 Db 183 gaaatctacatcgaagcaatgctgttctcctcgaacgttatcttgaagaaga 242  
 QY 1315 gattccaaagcggtgtgagtcgtcga 1340  
 Db 243 aattccagctgtgtgagtcgtcga 268  
 RESULT 10  
 AAA96460  
 ID AAA96460 standard; DNA; 207 BP.  
 XX  
 AC AAA96460:  
 XX 08-FEB-2001 (first entry)  
 DT  
 XX Nucleotide sequence of the promoter Mpi1048.  
 DE  
 KM petE promoter; chimeric promoter; transgenic plant; Mpi1047;  
 KM plastocyanin gene promoter; ss.  
 XX  
 OS Synthetic.  
 OS Pisum sativum.  
 XX  
 IN W0200056906-A1.  
 XX  
 PP 28-SEP-2000.  
 XX  
 PF 20-MAR-2000; 2000W0-1800317.  
 XX  
 PP 22-MAR-1999; 99FP-0003635.  
 XX  
 FA (MERIT) MERISTEM THERAPEUTICS.  
 XX  
 PI Rance I, Gruber V, Theisen M;  
 PI  
 PI  
 DR WPI; 2000-587667/55.  
 XX  
 PT Chimeric expression promoter for producing direct/inducous and  
 PT monocytotoxicous transgenic plants comprises a nucleic acid sequence  
 PT derived from a promoter of the pea plastocyanin gene  
 XX  
 PS Claim 2: Page 67; 83pp; English.









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ACCESSION	HGA57563
VERSION	HGA57563.1
KEYWORDS	EST
SOURCE	GI:13380804
ORGANISM	Dandel medic.
REFERENCE	Medicago truncatula
AUTHORS	Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
TITLE	1 (bases 1 to 637)
COMMENT	Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W., May,G.D., and Harrison,M.J. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library Unpublished (2006) Contact: Harrison MJ Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7325 Fax: 580 221 7360 Email: mharrison@noble.org Insert Length: 637 nt Error: 0.00 Plate: 105 row G column: 07 Seq primer: TCACACAGCAAAACACCATGAC. location/Qualifiers 1..637 /organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NP105C07P1." /cfeature="11b--Phosphate starved leaf" /tissue-type="leaf" /dev-stage="trifoliolate" /note="Vector: Lambda zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 200M potassium phosphate. RNA was prepared from above ground tissues."
BASE COUNT	178 a 148 c 128 g 182 t others 1
ORIGIN	
Query Match	32.1% Score 413.8; DR 10; length 637;
Best Local Similarity	95.4%; Pred. No. 1.2e-61;
Matches	472; Conservative 0; Mismatches 12; Indels 11; Gaps 2.
Q7	caaaaacccatcacactct... atccccctttctataaaadaaacatttgtagtc 505
D3	8 CAAAAACCATGCACATCTTATTCATCATCCATCTCTATAAAAATATACCTTTGGACGC 67
QY	tacctttgatctect caaacaatalaagaagaagat aa' anttaalcatcat 965
DB	68 TACTCTTCATTCCTTCATTATACATCATACAAACAGAACACAC-----TAATTAATCAT 119
QY	ccttgagaaaaatggcacccgtactcttcacacaccgctgcatttcacatccaagccc 1025
LB	120 CTTGAGAA-AAAAATGATTAAGTITATTTTAAACAATTTSTTAATTTAATCATTCGAAGAAT 179
CY	1026 tttaaggcaaaagcaagcaaatgtaaagcatagt taagtttcaattcaattcaat 1085
LB	180 TTAAAGCGCAAACGCCAAGCAAAAGTTACTGTCCATVAGGTAAAGCTTTCGAATTCGCAAT 239
CY	1086 tggcaagagcttttgtgaagagcttccctccaagaagatttggaattgtatgtatgtgcaagc 1145
LB	240 TGCCAAAGCTTTTGTGTCACAGCTTTTCCTCTAAACACATTTGGACATTTCTTCTTCTGACATC 299
QY	1146 ctgcaagatgcattgtatgctagcaaatgccctgtccatgtgaagtgatgtctgtatgtatgt 1205
DB	300 CTGTAAAGTTCATTTCTATCTATGTAAGAGCTTTGTGCTTGAAGCTCTCTTTGCTGCTAGTG 359
QY	atgggggtttgtgcttttgttccaaacaaatttcaagcttgcaagctctgtgagacacacattacat 1265

D6	360	ATGGGCGTTTGGCTTTTGTCGAACCAATTCCAGGTGCAGCAGCTGCACAFACCAT	419	
CY	1266	CAAGAACAACAGCGACTTCCTCACCAGTAACTTAATGAGAGAGAGAGAT	1325	
NB	420	TCAAACAATAATGTTGTTTTCTTAATACATATCTTTAAGSASAMSAATTCACAG	479	
OY	1326	GAGTAGAGCTGCCAA	1340	
DB	480	GAGTTGATGCAGCA	494	
RESULT	4			
H249400		483 bp	mRNA linear EST 21 Dec 2000	
LOCUS	NP014F06ELF1058	Developing leaf	Medicago truncatula cDNA clone	
DEFINITION	NP014F06EF 5' mRNA sequence.			
ACCESSION	BZ29400			
VERSION	BZ29400.2	G111959244		
KEYWORDS	EST.			
SOURCE	barrel medic.			
ORGANISM	Medicago truncatula			
Eukaryote:	Virdiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
Rosidae; eurosids I; Fabales; Papilionoideae; Trifoliales;				
Medicago.				
1 (bases 1 to 483)				
REFERENCE	Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,			
AUTHORS	Flores,H.R., Imman,T.T., Weller,J.W. and May,G.D.			
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation			
JOURNAL	Medicago truncatula leaf library			
COMMENT	Unpublished (2000) On Jul 13, 2000 this sequence version replaced gi:119461. Contact: May GD Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391 Fax: 580 221 7380 Email: gdmay@noble.org Medicago Genome Initiative accession: MGIS:14974 Insert Length: 671 Std Error: 0.00 Plate: 014 row: F column: 06 Seq primer: JCCACAGCAAGAACGCTATCAC. location/Qualifiers length=483 /db_xref="taxon:3880" /cclone="NP014F06E.F"          /cloned_lib="developing leaf" /tissue_type="leaf" /dev_stage="Pooled developmental" /note="Vector. Lambda ZAP. Contains a mixture of very young, developing, mature and senescing leaves." BASE COUNT     133 A     112 C     95 G     14 T ORIGIN			
FEATURES	Source			
Query Match	30.7%	Score 414.8;	DB 10; Length 483;	
Best Local Similarity	93.6%;	Pred. No 1 bn-58;		
Matches 457;	Conservative 0;	Mismatches 22;	Indels 9,	
Gap 2;				
D6	1	CTTATCTATCACTTATCAATATATAAAAAATCATCTTTGAGATATACCTTTTGATTCGCTT	60	
CY	923	CAACACATACCAAGAGAGAGAGACTAATTAATTAATATGATCTAGAGAGAAATAGCG	982	
NB	61	CAIACATATATCAAAAAGSADGAGAG-----TAAATATATCTGCAGCAAAATCGCC	112	
CY	983	AGCTTACTTCAAGAGAGTTTGTATTCACATCAACAGAGCTTAAGGATTAAGAGAGG	1042	
DB	113	ACCTTATCTTCAACCAAGCTTCCATTCATTCATTCATTCACAGGCTTAAGGCAAAACCGAAGC	172	

















[illegible]

RESULT 12  
 DTG 08-212 463 1470  
 Sequence 14, Application 10708, 12403  
 Patient No. 5670167  
 GENERAL INFORMATION:  
 APPLICANT: DARNER, F.  
 APPLICANT: SCHULTZ, J. F.  
 APPLICANT: FALKNER, F. G.  
 TITLE OF INVENTION: RECOMBINANT POLYOMAVIRUS

NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Policy & Law Unit  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM ps/compatile  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/87/945,413  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300,6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BERT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/CITATION NUMBER: 04/27/14 IMM  
TELEPHONE: (703) 983 9400  
TELEFAX: (703) 983 4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDINESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZ19-F15  
US-08-232,463-14





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DB      78 TAATAATTAACTAATAATTAATAAAAAAGTTTAACTTAACCTTTAAATTA
RBSJIT 6
US-98-998-416-1137
Sequence 1137, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Redischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHRAA CONSTITUTIVE
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264ar's Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NO. 6239264atf Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-Dec-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-Dec-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CCT1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1137:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1692RF
US-08-998-416-1137

Query Match          4.4%; Score 58.8; DH 4; Length 636;
Best Local Similarity 45.5%; Pred. No. 2.4e-05;
Matches 245; Conservative 0; Mismatches 292; Indels 1; Gaps 1

Q7      68 aaagtgtagcaattttatatttgaacaaataatcacactactagtgtgtaaaatcattat 127
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D3      6 AAATATATATTAATTAACTTAATTAATAACAATAATAAACCTTTTAAATAAATTAACG 65

Q7      128 aaacatagagctaaagaatatgatgataagaacaagagtagtgtatctttgcacaaa 187
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D3      66 ATTAATTAATTATTAACACTTAATTATTCATTATTTAAATAATTAAATTAATTGATTTATA 125

QY      188 ttgttcgaacactttgagaanaattgtgtctctctttccatctgttcgaacacata 247
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      126 CTATATATATTAATTATTAATTAATTAACCTTAATTCATCATTAATTAATTAATTATTA 185

CY      248 gaaggagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaag 307

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Db      186  TAAAATATATTTTAAATGAACTATTTCATCTATGTTTAAATTTAAATTTACTTAT 245
Qy      308  acaaaagttgacccaataatgtgacaatatcatcattgaagaaattgacaaagctaac 467
Db      246  AAAATATATATAGATATATTTATTTTCTTTAAATTAATTAATAA:ATATCAATAAT 305
Qy      368  aaalaagaagcttaattgcctgataaataaagaagagacgacattaaagaatgacctag 427
Db      306  AATATATATATTTATTAAT-TGTTTTATTAATAATAATATTTTATTTATTAATAAGCTTAA 464
Qy      428  agaatttllggaattcatlaaaaagaagaataatatttaaatlaaatlgaag 487
Db      365  TTATTTAAATATTTCTAAATTTATTTATTTATTAATAATCTATTTTAAATAATATG 424
Qy      488  tcaattgataaacacatgctgattttaatgaattgataagagattgaaataaattga 547
Db      425  TTGATTTATATTTATTTAAATCTTTTATTAAGAAATATTTATTAATAATTTAAATTTAA 484
Qy      548  ttaataatgaatllggtatlaaattlaattlaacattlaattcttllatataat 605
Db      485  TTCTTATATTTAAATTTTATTTATTTATTTAAATTAATAATTAATTCATTTTATTAAT 542

RESULT 7
US-08-446-855A-1
: Sequence 1, Application US/0844685A
: Patent No. 5849573
: GENERAL INFORMATION:
: APPLICANT: Stewart, Thomas S
: APPLICANT: Flores, Maria V
: APPLICANT: O'Sullivan, William J
: TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nixon & Vanderyhe PC
: STREET: 1100 No. 5849573th Glebe Road, 8th Floor
: CITY: Arlington
: STATE: Virginia
: COUNTRY: USA
: ZIP: 22201-4714
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patcom Release #1.24
: CURRENT APPLICATION DATA:
: APPL. ALIEN NUMBER: US/08-446-855A
: FILING DATE: 06-01-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Mitchard, Leonard C
: REGISTRATION NUMBER: 29,009
: REFERENCE/DOCKET NUMBER: 47-80
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-816-4000
: TELEFAX: 703-816-4100
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8920 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: genomic
US-08-446-855A-1

Query Match 1.2% Score 57.2; 3H 2; Length 8920;
Best local Similarity 46.1%; Prod No 0.00015;
Matches 226; Conservative 0; Mismatches 267; Indels 1; Gaps 1;
52 aaagattgaagtaagaaagatgatacatttatttgaacaaatataaacactact 111

```







CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,755A  
FILING DATE: 19-AUG-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,658  
FILING DATE: 30-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/657,584  
FILING DATE: 19-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Sallwaachik, David R  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: 0F114.C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1511 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Amsacta model entomopoxvirus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: complement (18..218)  
NAME/KEY: CDS  
LOCATION: complement (234..782)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 852..1511  
US-08-107-755A-8

Query Match 3.9%, Score 52, DB 1, Length 1511,  
Best Local Similarity 44.7%; Pred. No. 0.0014;  
Matches 298; Conservative 0; Mismatches 355; Indels 13; Gaps 2;

QY 51 taaagttlaagttacacagtgtagatatttattttaaacaacaaatattcactactac 110  
DB 615 TAATATATTTCCGTCATCATTTATTAATATTTATTAATAAATCAATATTAATG 674  
QY 111 tgttaaacatcatattacatagagtaagaataatgatgatgaacacagtag 170  
DB 675 AGTTATATTTACACATTTTGTATGTATTAATAATATATTTATTTTGTGATTAAT 734  
QY 171 tgaatcttgacacacatattgtgtcaacattga-----gaaatllgtgttc 221  
DB 735 TGTGTGTTTGCAGAAACATAGGACCAATTAATTTCTATTCGACATTTTATTAATA 794  
QY 222 tctcttllcatlgtgccaagaacalagagaggaaggaaggaaggaaggaaggaat 281  
DB 795 TTTGATATATTTTTCATAAAAAAATTAATCAATGAAAAAATAAATTAATCAAAATG 854  
QY 282 aatgtagatagagagagaagttgtacaaagttgtacaaatagttgtacaaatc 341  
DB 855 GATTACTAAATTCGATTAATTTTAAATTAATTTTAAATTAATTTTAAATTAATAAAA 914  
QY 342 attgagaatttgacaaagctacacaaataaggttaattgctgtaataaataagat 401  
DB 915 ATATATTAATTAACAGACATTAATCTTAATTAATTAATTAATTAATTAATTAATTA 974  
QY 402 gacgcattagagagatgacacallagagatlllgtgcaagtcattaaagaagaagata 461  
DB 975 GAAGCAATTCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1034  
QY 462 aattattttaaatataaagttgagtcattgtatcaacatgtagatatttgaatt 521  
DB 1035 AAAAGTTTATATTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATA 1094

QY 522 gataagaagattgatataaagttgattagatattgaatttgaatgcaatttaattg 582  
DB 1095 AATATACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1154  
QY 582 acatttgatcttctctataatattcccaataagaataaataatgatttataatga 641  
DB 1155 CACATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1210  
QY 642 tagatcaataagaagaataacggtatattatccctccaaagaaagaaaggtatatt 701  
DB 1211 TATTAATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTG 1270  
QY 702 tactaa 707  
DB 1271 TAATAA 1276

RESULT 13  
US-08-544-332-8  
Sequence 8, Application US/08544332  
Patent No. 5935777  
GENERAL INFORMATION:  
APPLICANT: Koyet, Richard W.  
APPLICANT: Hall, Richard L.  
APPLICANT: Gruidl, Michael E.  
TITLE OF INVENTION: No. 5935777-1 Intcom-poxvirus Expression System  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gerard H. Bengen  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patella Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/544,332  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,867  
FILING DATE: 07-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/107,755  
FILING DATE: 19-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 92/14818  
FILING DATE: 12-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,685  
FILING DATE: 30-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/657,584  
FILING DATE: 19-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Bengen, Gerard H.  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: 0F114.C4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1511 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)







GenCorp version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2002 00:54:34 : Search time 413.71 seconds  
(without alignments)  
4941.301 Million cell updates/sec

Title: US-09-678-303-2  
971  
Perfect score: 1 cggcgcqataltatataatg.....aatcatcttgaagaataac 971  
Sequence:

Scoring table: IDENTITY\_NUC  
Gapop 10.0 : Gapext 1 0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 98  
Maximum Match 100%  
Listing first 45 summaries

Database : GenBank  
1: gb\_ba:\*  
2: gb\_hlq:\*  
3: gb\_in:\*  
4: gb\_un:\*  
5: gb\_ov:\*  
6: gb\_pal:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_la:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_com:\*  
21: em\_ot:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hq\_hum:\*  
31: em\_hq\_in:\*  
32: em\_hq\_other:\*  
33: em\_hqgo\_inv:\*

Prod No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result Query  
No. Score Match Length DB ID Descr:Plon

1	971	100.0	971	6	AX105268	AX105268 Sequence
2	971	100.0	1350	6	AX105267	AX105267 Sequence
3	731	75.8	731	6	AX105269	AX105269 Sequence
4	191.8	19.8	623	6	AX036596	AX036596 Sequence
5	191.8	19.8	834	6	AX036595	AX036595 Sequence
6	189.6	19.5	326	6	AX036597	AX036597 Sequence
7	179.4	18.5	998	6	PSDET	PSDET
8	179.4	18.5	1505	8	ESTLAS	ESTLAS
9	128.2	13.2	1716	8	ALPBPV	ALPBPV
10	128.2	13.2	1716	8	MSU18296	MSU18296
11	116	11.9	207	6	AX036598	AX036598 Sequence
12	107.5	11.1	64590	8	AV087771	AV087771
13	106.4	11.0	250	6	AX036600	AX036600 Sequence
14	89.4	9.2	281	6	AX036599	AX036599 Sequence
15	89	9.2	280	6	AX036601	AX036601 Sequence
16	89	9.2	296	6	AX046603	AX046603 Sequence
17	89	9.2	296	6	AX036602	AX036602 Sequence
18	88.4	9.1	220	6	AX036604	AX036604 Sequence
19	85.8	8.8	22243	3	EPVAVAR23A	EPVAVAR23A
20	84.2	8.7	67970	3	PEMALIP3	PEMALIP3
21	84.2	8.7	151032	2	AC105201	AC105201
22	81.8	8.4	170141	2	AL611928	AL611928 Homo sapi
23	81.2	8.4	310721	2	AL627107	AL627107 Homo sapi
24	80.8	8.3	92487	9	AL592166	AL592166 Human DNA
25	79.6	8.2	1987	3	LDIRAP1A	LDIRAP1A
26	79.2	8.2	296	6	AL2982	AL2982
27	78.8	8.1	93140	2	AC106215	AC106215
28	78.8	8.1	171195	2	AC095822	AC095822
29	78.5	8.1	139801	3	AC094212	AC094212 Drosophila
30	77.4	8.0	156723	3	AC010838	AC010838 Drosophila
31	77.2	8.0	2503	6	AX033851	AX033851 Sequence
32	77.2	8.0	130117	6	AC004407	AC004407 Homo sapi
33	76.8	7.9	155705	2	AC105451	AC105451 Homo sapi
34	76.8	7.8	259	6	AX046610	AX046610 Sequence
35	76	7.8	158950	9	AL329125	AL329125 Human DNA
36	75.8	7.8	165794	2	AC094468	AC094468 Plasmid
37	75.6	7.8	172805	9	AC066608	AC066608 Homo sapi
38	75.4	7.8	104992	2	AC005504	AC005504 Plasmid
39	75.4	7.8	169546	2	AC004157	AC004157 Plasmid
40	75	7.7	14867	3	AC001398	AC001398 Plasmid
41	75	7.7	154995	9	AC011979	AC011979 Homo sapi
42	74.8	7.7	84563	5	AC096885	AC096885 Dario fer
43	74.6	7.7	92492	2	AL672088	AL672088 Dario fer
44	74.4	7.7	7597	6	AX345915	AX345915 Sequence
45	74.2	7.6	80827	3	EPMA3095	EPMA3095 Plasmid

## ALIGNMENTS

RESULT 1  
AX105268  
FACTS  
DEFINITION Sequence 2 from Patent WO0125455  
ACCESSION AX105268  
VERSION AX105268.1 GI:13921418  
KEYWORDS  
ORGANISM  
SOURCE  
REFERENCE  
1 (bases 1 to 971)  
AUTHORS  
TITLE  
JOURNAL  
Medicago Inc. (CA)  
Location/Qualifiers  
1..971  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Sequence to be used as a Promoter for regulating expression"

BASE COUNT 390 a 141 c 145 g 295 t  
ORIGIN



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Db 609 CATTAGAGTCAATTAATTAATTATTTATAGATTAATATAGAAATAGAGAAATAGAGATAT 668
QY 661 attaatccctcccaaaaaaaacggtatattactaaaaatcaaacacggtatgag 720
Db 669 ATTAACTCCCTCAAAAAAAGGATATATTTACTAAAAAAATCAAGCCACGTAAGAG 728
QY 721 gataaatccaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaac 780
Db 729 GATAACATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAA 788
QY 781 gcaactctgtgacacatctacatctacatctacatctacatctacatctacatctac 840
Db 789 GCACCTGTGTGACACATCTACATCTACATCTACATCTACATCTACATCTACATCTAC 848
QY 841 caaaacccaacacacacacacacacacacacacacacacacacacacacacacacacac 900
Db 849 CAAAAACCAATCCACATCTTATACCCCATCTATATAAAAAATCACACTTTGTACCTAC 908
QY 901 acttgatccctcccaaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaac 960
Db 909 ACTTGATCCCTCCCAAAACCAATCCAAAGAGAGACATTAATTAATTAATTAATTAAT 968
QY 961 gagagaaagt 971
Db 969 GAGAGAAAGT 979

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RESULT 3
AX105269 731 bp. ENA 110039 FAT 30-APR-2001
LOCUS AX105269
DEFINITION Sequence 3 from Patent W00125405.
ACCESSION AX105269
VERSION AX105269.1 GI:13921419
KEYWORDS
ORGANISM synthetic construct.
SOURCE synthetic construct.
REFERENCE 1 (bases 1 to 731)
AUTHORS Verma, P. and Agrawal, M. A
TITL E Promoter for regulating expression of foreign genes
JOURNAL Patent: WO 0125405-A 3 12-APR-2001;
Medicago Inc. (CA)
FEATURES
Source location/Qualifiers
1..731
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Sequence to be used as a promoter for regulating
expression"
BASE COUNT 299 a 113 c 109 g 210 t
ORIGIN

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Query Match 75.3%; Score 731; DB 6; Length 731;
Best Local Similarity 100.0%; Pred. No. 4 6e-107
Matches 731; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 241 agagagagagagagagagagagagagagagagagagagagagagagagagagagagag 300
Db 1 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 301 caaaagctgacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaac 360
Db 61 CAAAAGCTGTACCAAAATACTTCTACAAATATCTATTCAGCAATTTTACCAAAAGCTACACA 120
QY 361 aataagagtaattgctgtaataataaagagagagagagagagagagagagagagagagag 420
Db 121 AATAAGGTTAATGTGTAAATTAATTAAGGATTAATTAAGGATTAATTAAGGATTAATTA 180
QY 421 gaatttggcaagctaaagagagagagagagagagagagagagagagagagagagagagag 480
Db 181 GAATTTTGGCAAGCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 481 callgatalaacaatgatalatataagatgataaagatgatalaagatgatal 540

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Db 241 CATTGATTAACATGTATATTATTAATGAAATGATTAAGAGTGAATTAAGTTATAT 300
QY 541 tagtaattagaatttggtgtcgaatttaattggaatttgatctttctctctctctctct 600
Db 301 TAGTAATTAGAATTGTTGTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
QY 601 ccaagagatgacatgacatgacatgacatgacatgacatgacatgacatgacatgacatg 660
Db 361 CCATAGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATG 420
QY 661 attaatccctcccaaaaaaaacggtatattactaaaaatcaaacacggtatgag 720
Db 421 ATTAACTCCCTCAAAAAAAGGATATATTTACTAAAAAAATCAAGCCACGTAAGAG 480
QY 721 gataaatccaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaac 780
Db 481 GATAACATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAAATCCAA 540
QY 781 gcaactctgtgacacatctacatctacatctacatctacatctacatctacatctac 840
Db 541 GCACCTGTGTGACACATCTACATCTACATCTACATCTACATCTACATCTACATCTAC 600
QY 841 caaaacccaacacacacacacacacacacacacacacacacacacacacacacacacac 900
Db 601 CAAAAACCAATCCACATCTTATACCCCATCTATATAAAAAATCACACTTTGTACCTAC 660
QY 901 acttgatccctcccaaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaac 960
Db 661 ACTTGATCCCTCCCAAAACCAATCCAAAGAGAGACATTAATTAATTAATTAATTAAT 720
QY 961 gagagaaagt 971
Db 721 CACAGAAAGT 731

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RESULT 4
AX036596 623 bp. ENA 110039 FAT 15-NOV-2000
LOCUS AX036596
DEFINITION Sequence 2 from Patent P42791358
ACCESSION AX036596
VERSION AX036596.1 GI:11226191
KEYWORDS
ORGANISM synthetic construct.
SOURCE synthetic construct.
REFERENCE 1 (bases 1 to 623)
AUTHORS Rance, J., Theisen, M. and Gruber, V.
JOURNAL Patent: FR 2791358-A 2 29-SEP-2000;
MERISTEM THERAPEUTICS (FR)
FEATURES
Source location/Qualifiers
1..623
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MP1097 derived from the promoter pte1 by
a deletion in 5' of the repeated invert sequences as well
as the as 1 like box borne on fragment Spl1 of 212 bp
promoter MP1097"
BASE COUNT 230 a 128 c 82 g 183 t
ORIGIN
Query Match 19.8%; Score 191.8; DB 6; Length 623;
Best Local Similarity 82.8%; Pred. No. 1 9e-213
Matches 231; Conservative 0; Mismatches 47; Indels 1; Gaps 1;
QY 673 aaaaaaaacggtatattactaaaaatcaaacacggtatgag 732
Db 321 AATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 380
QY 733 tcaaacatcgaacacacacacacacacacacacacacacacacacacacacacacacacac 792

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**COMMENT**  
At 1 is a plant nuclear protein binding to the sequence AATAATATAT in the promoters of light-regulated genes (N. Jaffe & A.R. Cashmore: binding of a pea nuclear protein to promoters of

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**1**

1



BASE COUNT 576 a 286 c 298 g 556 t  
ORIGIN

VPKDIVPEWRIEFSAAATGAFEAHDIRWYSFHSSELIVFNNNNANVSSVQTA"

Query Match 13.2%; Score 128.2; DB 8; Length 1716;  
Best Local Similarity 81.8%; Pred. No. 1.9e-11;  
Matches 148; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 156 agagtgatgatatttgaaacaaatttcttgacatttgagaaatttctgtgtctc 215  
DB 97 AGAGTATGATATTGAAACCAATTCATGAAACCTTGTGAACCTGTGTTCTTC 156  
QY 216 tcttctcatgtgcaaaatcaatagagagagagagagagagagagagagagag 275  
DB 157 ATTCTTATTTGTCAAAACAAATGACAGAGAGAGAGAGAGAGAGAGAGATATCA 216  
QY 276 tctgagatagagagagagagagagagagagagagagagagagagagagag 335  
DB 217 TGTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATATCA 276  
QY 336 t 336  
DB 277 T 277

RESULT 11  
LOCUS AX036598 207 bp. FNA linear PAT 16-NOV-2000  
DEFINITION Sequence 4 from Patent FR2791358.  
ACCESSION AX036598  
VERSION AX036598.1 GI:11226193  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 207)  
AUTHORS Rance, L., Theisen, M. and Gruber, V.  
JOURNAL Patent: FR 2791358-A 4 29-SEP-2000;  
MERISTEM THERAPEUTICS (PK)

FEATURES  
source  
1..207  
Location/Qualifiers

Promoter  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

/note="The promoter Mpr1098 of 207 bp only contains the  
"TATA" and "CAAT" boxes and corresponds to a minimal  
reference promoter on the promoter file  
Promoter Mpr1098"

BASE COUNT 67 a 58 c 21 g 61 t  
ORIGIN

Query Match 11.9%; Score 116; DB 6; Length 207;  
Best Local Similarity 84.5%; Pred. No. 2.5e-09;  
Matches 142; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

QY 784 cctctgagacacatcatatctaaabacacattcttcacacatcttgagagagag 843  
DB 16 CTCTGTGGCAGCATTCATATTCATATTCATATTCATATTCATATTCATATTCAT 75  
QY 844 aa-ccaatcacatctctatcccatctatataaaatcacatcttgagagagag 902  
DB 76 AAACCCATTCACATCTTATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 135  
QY 903 ttgatccctcaaacacacacacacacacacacacacacacacacacacacacac 950  
DB 136 TTGATTCCTCTCAACACATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 183

RESULT 12  
AC087771/c 69590 bp DNA linear PLN 13-APR-2001  
LC005

DEFINITION Genomic Sequence for Medicago truncatula, clone RD15, complete  
sequence.  
ACCESSION AC087771  
VERSION AC087771.3 GI:14717388  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
1 (bases 1 to 69590)  
Huang, E., de la Bastide, M., Nascimento, L., Spiegel, L., Kirchhoff, K.,  
Proctor, F., King, J., Zlatavsky, I., Santos, L., Miller, B., Kuhl, R.,  
Cunius, D. M., Bell, M., Ballja, V., Shah, R., Haber, A., Yang, C.,  
Palmer, L., O'Shaughnessy, A., Dedhia, N., and McCombie, W. R.  
Genomic Sequence for Medicago truncatula, clone RD15, complete  
sequence

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Submitted (23-JAN-2001) Lila Annenberg Hazen Genome Sequencing  
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring  
Harbor, NY 11724, USA  
3 (bases 1 to 69590)  
McCombie, W. R.  
Direct Submission  
Submitted (30-JUN-2001) Lila Annenberg Hazen Genome Sequencing  
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring  
Harbor, NY 11724, USA  
4 (bases 1 to 69590)  
Huang, E., de la Bastide, M., Spiegel, L., Nascimento, L., Kirchhoff, K.,  
Proctor, F., King, J., Zlatavsky, I., Santos, L., Miller, B., Kuhl, R.,  
Cunius, D. M., Bell, M., Ballja, V., Shah, R., Haber, A., Yang, C.,  
Dix, S., O'Shaughnessy, A., Palmer, L., Dedhia, N., and McCombie, W. R.  
Direct Submission  
Submitted (13-JUL-2001) Lila Annenberg Hazen Genome Sequencing  
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring  
Harbor, NY 11724, USA

COMMENT  
on Jul 13, 2001 this sequence version replaced at:14578148  
This sequence was finished as follows unless otherwise noted: all  
regions were either double stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >=  
30), an attempt was made to resolve all sequencing problems, such  
as compressions and repeats, all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest.

FEATURES  
source  
1..69590  
Location/Qualifiers

misc\_feature  
/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/clone="8015"  
47170..47550  
/note="The sequence is covered by multiple subclones  
derived from a PCR product amplified with a high fidelity  
polymerase. The sequence is of high quality."  
47550..48613  
/note="The sequence is covered by a PCR product which was  
amplified with a high fidelity polymerase and by 2 M13  
subclones. The sequence is high quality."  
48613..48750  
/note="The region is covered only by PCR products which  
were amplified with a high fidelity polymerase and  
sequenced with both dye terminator and GTP terminator  
chemistries."  
48750..49160  
/note="The sequence is covered by a PCR product which was  
amplified with a high fidelity polymerase and one M13  
subclone. The sequence is high quality."  
49160..49270  
/note="The region is covered only by a PCR product which  
was amplified with a high fidelity polymerase, as well as

misc\_feature

misc\_feature

misc\_feature











```

OY 181 ttgttgcacattgagaaatttgtttctctcttcattgtgcacaaagatag 240
    |||||||
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OY 241 agagagaaagagagagagagagagagagagagagagagagagagagag 300
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Db 249 agagagaaagagagagagagagagagagagagagagagagagagagag 308
OY 301 caaaattgtaccgaatattgttgcacatattgttgcacaaagatag 360
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OY 361 aataagagatattgttgcacaaatagagagagagagagagagagagag 420
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OY 421 gaattttgcaagtcattaaagagagagagagagagagagagagagag 480
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OY 481 cattgattaaacatgatttatttgaagatgagagagagagagagagag 540
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OY 601 cctagagtcagtaattacatttatttatttcatagatgcacaaagagagat 660
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OY 661 attaatccctcccaaaaaaaacgqatatttactaaanaactgaagcagtag 720
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OY 841 caaaacccaatccaatccattatccacatttataaaacacacatttgcac 900
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Db 849 caaaacccaatccaatccattatccacatttataaaacacacatttgcac 908
OY 901 acttgcattcccttcaacacacacacacacacacacacacacacacac 960
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Db 969 gagagaaatg 979

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RESULT 3
ID AAS02128
XX AAS02128 standard, DNA, 731 bp.
AC AAS02128:
XX
XX 18-JUL-2001 (first entry)
XX
XX Promoter #3 for regulating expression of foreign genes.
XX
XX Promoter, transgenic plant, monocotyledon; dicotyledon; gymnosperm; ds.
XX
XX Synthetic.
XX
XX WO200125455-A2.
PN

```

```

XX
XX 12-APR-2001.
XX
XX C2-OCT-2000; 2000W CA01144.
XX
XX 04-OCT-1999; 99US-0157124.
XX
XX (MEDT-) MEDICAGO INC.
XX
XX Velina L. F'roust M.
XX
XX WPI: 2001-266315/27.
XX
XX Novel promoter for regulating expression of foreign genes in transgenic
XX plants, more specifically in a leaf-specific manner in transgenic
XX plants.
XX
XX Claim 1; Page 9; 9pp; English.
XX
XX The sequence represents the coding sequence of promoter #3 for regulating
XX expression of foreign genes in transgenic organisms. The promoter is
XX useful for regulating the expression of foreign genes in transgenic
XX organisms, particularly plants, e.g. monocotyledons, dicotyledons or
XX gymnosperms, by preparing a transgenic organism using an expression
XX construct comprising the promoter and an open reading frame (ORF) of a
XX gene.
XX
XX Sequence 731 BP; 299 A; 113 G; 109 G; 210 T; 6 other.
XX
Query Match 75.3%; Score 731; DB 22; Length 731;
Host Local Similarity 100.0%; Proc. No. 3,5e-121;
Matches 731; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    |||||||
Db 1 agagagaaagagagagagagagagagagagagagagagagagagagag 60
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    |||||||
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    |||||||
Db 121 aataagagatattgttgcacaaatagagagagagagagagagagagag 420
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    |||||||
Db 181 gaattttgcaagtcattaaagagagagagagagagagagagagagag 480
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Db 421 aataagagatattgttgcacaaatagagagagagagagagagagagag 420
OY 481 gataacatccaatccaacatccaacatcccgatgagatgaacccaattga 780
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Db 541 gcaactgtggcagtcacattatcatatcatatcatatccacatttcagac 840

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[illegible]









RECORDS DEFINITION	464 bp 11,274,545bp	RNA Modificate Tromaculua BAC <sup>+</sup> library 2,00K11, RNA sequence <sup>+</sup>	11,000 BAC to Atp <sup>+</sup>	155 to Atp <sup>+</sup>
RE001091				

ARTICLE VERSION KEYWORDS SOURCE	BARCEL MEDIA
ARTICLE VERSION KEYWORDS SOURCE	BARCEL MEDIA

ORGANISM

**REFERENCE**  
**AUTHORS** 1 1 (bases 1 to 64)  
**TITLE** Pomeroy, R. V., Abo, J. M., Jordan, J. L., and Cook, L. K.  
**JOURNAL** *Environ Biol Fish* 1991; 30: 1-10  
**INPUT/SHED** (2001)  
**CONTACT**: Cook, Jp  
**COMMENT**  
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[illegible]

753-000113 *Medicines Terminology Library* / *Pharmacovigilance Photobank*: Site 1: *Handbook* 2: *Handbook 3*. Nam, Y. M., Christensen, E. V., Eide, J., Kim, I., and Cook, D. R. 1999. Construction of a hierarchical artificial chromosome library of Medicines Terminology and identification of clones containing cytochrome response genes. *Proc Appl Genet* 48: 64-66. \*response

Direct Match:	19.48;	Score: 100.4;	Pos: 1.2;	Length: 46.4;
Fast Local Similarity:	81.78;	Prod. No. 6.4e-06;		
Matches: 19;	Conservative: 0;	Missed Matches: 29;	Isotopes: 0;	Caps: 0;

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VERSION	HM001085
KEYWORDS	AB001085.1 51:1387196
SOURCE	GENS.
	partial modified

ORGANISM  
Medicamentum  
Eukaryotic: Viridiplantae: Streptophyta: Embryophyta: Equisetum  
Spermatophyta: Magnoliophyta: Equisetum: Equisetum





filters for hybridization from the HACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

Location/Qualifiers

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/organism="Drosophila melanogaster"

/db\_xref="taxon:7227"

/clone\_lib="RPL-98"

/clone="BACR08K10"

/note="end: TERT3"

BASE COUNT 201 a 64 c 131 g 202 t 503 o.hers

ORIGIN

Query Match 10.0%; Score 97; DB 12; Length 1101;

Best Local Similarity 24.0%; Pred. No. 1.5e-05;

Matches 122; Conservative 208; Mismatches 170; In P's 9; Gaps 1;

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QY 42 ataaagtttaagttgacagagtggtacattttatttgaacaaaaattccacta 101
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Db 903 AADDTDCTKIDJDKWDJMKAKGFWGDAWMAATDMMWMCWADWMTWDAADWW 844
QY 102 ctgtataaalcattlaaacolltaaglaaagaalalggatgalaagaagaqla 161
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Db 843 AADRWDMAMKWDAMAMGAPTAHPWGPACRPGCAKRPKPKPAADKPIAADPDNA 784
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Db 783 ATTTTWTTTTTRDDBDKKKTDTWTFWAADPTWDPDDDDPDPACTAGPKKPTWKPRK 724
QY 222 catgtgtcaaaaacaatajagagagaaa..... jaggagagagagataaaga 272
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Db 723 KPIPLWMLALADPLAMLDKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPK 664
QY 273 taatgtagatagagagaaagttgacaaagttgacaaatagttgacaaatat 332
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Db 663 TTTTDTDDMDKRRKRRKRRRTTARAAMWMTKAMWMAKMWKTPADWNPWMAAP 604
QY 333 catlgaggaaattgacaaagctacacaaataagggtlaattgctgaataaaga 392
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Db 603 TWIDAFKADRWAKAFAMZAPDPAPAPAPDPWTTKGKTTTATWTTWAAFAAMW 544
QY 393 tgaagcatlgagagatgacattagagaatttgcgaagtcattaaagaagaat 452
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Db 543 ATTTATWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTT 484
QY 453 aaatlattltaaattlaaagttgaatcattgaatlaaacaalgaattlaaagaat 512
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Search completed: August 31, 2002, 23:45:47  
Job time: 19093 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Pur on. September 1, 2002, 00:57:11 Search time: 06:05:59:00:00  
(without alignments) 2483.187 Million cell updates/sec

Title: US-09-678-303-2

Perfect score: 971

Sequence: 1 cgagcgtatattatattatg...

Scoring table: IDENTITY NUC Gapop 10 0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued\_Patents\_NA:\*

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2: /cgn2\_6/plodata/1/ina/5B.COMB.seq:\*\*

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6: /cgn2\_6/plodata/1/ina/5B.COMB.seq:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	68.2	7.0	19124	2	US-08-487-826B-13
2	66.4	6.8	7218	1	US-08-232-463-14
3	65.8	6.8	837	4	US-08-998-416-288
4	61.8	6.4	615	4	US-08-998-416-186
5	61	6.3	615	4	US-08-998-416-186
6	58.8	6.1	636	4	US-08-998-416-1137
7	57.2	5.9	8920	2	US-08-446-855A-1
8	57.2	5.9	8920	2	US-09-150-741-1
9	54.6	5.6	19124	2	US-08-487-826B-13
10	53.2	5.5	636	4	US-08-998-416-1137
11	52	5.4	1511	1	US-07-991-867B-8
12	52	5.4	1511	1	US-08-107-755A-8
13	52	5.4	1511	2	US-08-544-332-8
14	51.8	5.3	837	4	US-08-998-416-288
15	48.8	5.0	658	4	US-08-998-416-595
16	48.2	5.0	6124	4	US-08-213-419B-3
17	48	4.9	2317	3	US-08-749-522-5
18	48	4.9	3974	4	US-08-667-504-3
19	47.6	4.9	863	4	US-08-998-416-498
20	47.2	4.9	6243	2	US-09-056-075-1
21	46.6	4.8	5852	1	US-07-867-106-2
22	46.2	4.8	665	2	US-08-883-795A-36
23	45.8	4.7	5852	1	US-07-867-106-2
24	45.6	4.7	731	1	US-08-451-405A-2
25	45.4	4.7	6768	1	US-08-107-755A-1
26	45.4	4.7	8457	1	US-07-991-867B-1
27	45.4	4.7	8457	2	US-08-544-332-1

28	45	4.6	1186	2	US-08-731-722-5	Sequence 5, Appl 1
29	44.6	4.5	2251	4	US-08-941-677-11	Sequence 11, Appl 1
30	44.5	4.5	4045	6	US-08-168-1	Sequence No. 5, Appl 1
31	44.4	4.5	3529	4	US-08-984-320-3	Sequence 2, Appl 1
32	44.4	4.6	3528	4	US-08-487-087A-2	Sequence 2, Appl 1
33	44.4	4.6	4383	6	US-08-397-653B-2	Sequence 2, Appl 1
34	44.4	4.6	4383	6	US-08-397-653B-2	Sequence 2, Appl 1
35	44	4.5	9535	1	US-08-323-173B-1	Sequence 1, Appl 1
36	44	4.5	9636	4	US-08-954-441-1	Sequence 1, Appl 1
37	43.6	4.5	3350	3	US-08-617-860B-3	Sequence 3, Appl 1
38	43.4	4.5	740	4	US-08-998-416-971	Sequence 971, App
39	43.4	4.5	948	4	US-08-122-400B-5	Sequence 5, Appl 1
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41	42.8	4.4	731	1	US-08-451-405A-2	Sequence 2, Appl 1
42	42.8	4.4	3995	6	US-08-397-653B-2	Sequence 2, Appl 1
43	42.8	4.4	6243	2	US-09-056-075-1	Sequence 1, Appl 1
44	42.8	4.4	8920	2	US-08-446-855A-1	Sequence 1, Appl 1
45	42.8	4.4	8920	2	US-09-150-741-1	Sequence 1, Appl 1

## ALIGNMENTS

RESULT 1  
US-08-487-826B-13  
Sequence 13, Application US/08487826B  
Patent No. 5993827  
GENERAL INFORMATION:  
APPLICANT: Shim, Kim L.  
APPLICANT: Chitnis, Chetan  
APPLICANT: Miller, Louis H.  
APPLICANT: Peterson, David S.  
APPLICANT: Su, Xin-zhuan  
APPLICANT: Williams, Thomas E.  
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Knobbe Martens Olson & Bear  
STREET: 620 Newport Center Drive  
CITY: Newport Beach  
STATE: California  
COUNTRY: US  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,826B  
FILING DATE: 10-SEP-1993  
CLASSIFICATION: A35  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelson, Ned  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: NH121,001CP1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19124 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
EXTRACTED: NO  
ANTI-SENSE: NO  
US 08 487-826B-13  
Query Match 7.0% Score 68.2 DB 2 Length 19124







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; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jürgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Redischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPHII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwal Is Road
; CITY: Research Triangle Park
; STATE: NO. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #10, Version #130
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC- 97
; CLASSIFICATION: A35
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: JP/5-30306/A/CGP1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8487
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 1137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAC1692RP
; US-98-998-416-1137

Query Match          6.1% Score 58.8; DN 4; Length 636;
Blast Local Similarity 45.5%; Pred. No. 0.00036;
Matches 245; Conservative 0; Mismatches 292; Indels 0; Gaps 1;

OY      60 aaatgtagcatcttttat tgaacaaataaacacctactactgtgttaaaacatattt 119
DB      6 AAATATATATATTTAAAT TTAAAGAAGATTAAATGAACCTTTTATTTAATTAATTTAACT 65

OY      120 aaagcttgagtaaagaatatatgatgatgaagaacaagagttagtataatttgacaaca 179
DB      66 ATTAATATTATTTAAAGTATTTATATCATATTATTTAAATTAATTAATTTATGTGATTATTAATA 125

OY      180 ttatttcgaacatttgagaaatttgtgtgcctcctttcaattgtgtcaaaaacaata 239
DB      126 CTATATATATATATTAATTAATTAATTAATTTACTTAATTCATCATTAATTAATTAATTAATTA 185

OY      240 gaagagagaaaaagagagagagagaaataaacaataatgtatgagatagagagagaaagtttat 299
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[illegible]

```

1  RESULT 7
2  US-08-446-855A-1
3  Sequence 1, Application US/08446855A
4  Patent No. 5849573
5  GENERAL INFORMATION:
6  APPLICANT: Stewart, Thomas S
7  APPLICANT: Flores, Maria V
8  APPLICANT: O'Sullivan, William J
9  TITLE OF INVENTION: Nucleotide sequence encoding carnomyo-
10 TITLE OF INVENTION: phosphate synthetase II
11 NUMBER OF SEQUENCES: 2
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: Nixon & Vandertyne PC
14 STREET: 1100 No
15 CITY: Arlington
16 STATE: Virginia
17 COUNTRY: USA
18 ZIP: 22201-4714
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: Patent Release #1.24
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: 08/086446, 855A
26 FILING DATE: 06-Jul-1995
27 CLASSIFICATION: 435
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Mitchell, Leonard C
30 REGISTRATION NUMBER: 29,009
31 REFERENCE/DOCKET NUMBER: 47-80
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 703-816-4000
34 TELEFAX: 703-816-4100
35 INFORMATION FOR SEQ ID NO: 1:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 8920 base pairs
38 TYPE: nucleic acid
39 STANDARDS: Single
40 TOPOLOGY: linear
41 MOLECULE TYPE: genomic
42 US-08-446-855A-1
43
44 Query Match 5.9% Score 57.2; IH 2; Length 8920;
45 Host Local Similarity 46.1%; Prod No. 0.0012;
46 Matches 226; Conservative 0; Mismatches 263; Indels 1; Gaps 1;
47
48 44 aaaaatttaattagcaattttgacattttatagaacaaatatttcaactact 103

```

[illegible][illegible]

DB	5479	lqf laa q t a c t a g u a a t q a t a c q a a a a a c q u a a q a t a l a u a t a c t a c a a q u a t t	5568
UY	164	q a t a t t t q u a c a c a a t t t t q t q c a a t t t q a a a a t t t t q t q t e t e t t t t a	245
DB	5539	t a t q a a q a t c a a a a t q a t a t a a t a a q a t a a a a a a a t t t t t a t t a	5597
UY	224	t t q t c a a a c a t a q u a q a a a a a a a a a q t a a a t a a a a a a a t q a q a	285
DB	5598	a a q t q a t q a a a a a t t q t q a t q t a a t t a a a a a q u a a a t a a t t a t a a t q	5657
UY	284	t q a q a q a a a t t q t a c a a a a t t a t a c a a a a t a t q a a a a t a c t a q a a a t	345
DB	5658	t a a t a a t a a t q a q t q l a q q a a a a q a t a l q a t q a a a a a t a l a a t q a a t	5717
UY	344	t t q a a a a a a t t a c a a a a t a a q q t t a a t q t q t a a a a a t a a a a t a a q a t a a	405
DB	5718	q t a a a a c a t a l a a a a a a t a a a t a a a q a t a q a a t a a a t a a t a a t a q a a t q	5777
UY	404	a a a a t q a a a t t a a a a t t t t q a a a t c a t a a a a a a a a a a a t t t t	465
DB	5778	a g t t a c c a t q a a a c a t c a c a t c a a c t a a t q a t c a t t a t a t t o a a t t t a a t a	5837
UY	464	a a a a t t a a a t t a a t c a t t t q a t t a a a t a t q a t t a t t a a t a a t q a a a q a	525
DB	5838	c a t c a q a t q a a a a t a a q a a t a a t a a a a t a t q a a t a t t a c t a a q a a a a	5897
UY	524	t t q a t a a a	535
DB	5898	a t a t a t c t a a	5907

1 RESULT 9  
2 US 08 487 826H 13/1  
3 Sequence 13, Application US/08487826H  
4 Patent No. 5993627  
5  
6 GENERAL INFORMATION:  
7 APPLICANT: Sim, Kim L.  
8 APPLICANT: Chlunis, Chetan  
9 APPLICANT: Miller, Louis H.  
10 APPLICANT: Peterson, David S.  
11 APPLICANT: Su, Xin zhaun  
12 APPLICANT: Wellens, Thomas E.  
13 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
14 TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM EPITHELIAL BINDING PROTEINS  
15 NUMBER OF SEQUENCES: 45  
16  
17 CORRESPONDENCE ADDRESS:  
18 ACCESSIBLE: CROSBY MATTHEWS WILSON & BOAT  
19 STREET: 620 Newport Center Drive 16th Floor  
20 CITY: Newport Beach  
21 STATE: California  
22  
23 COUNTRY: US  
24  
25 ZIP: 92660  
26  
27 COMPUTER READABLE FORM:  
28 MEDIUM TYPE: Floppy disk  
29 COMPUTER: IBM pc compatible  
30 OPERATING SYSTEM: PC-DOS/MS-DOS  
31  
32 SOFTWARE: Patent in release #1.0, Version #1.25  
33  
34 CURRENT APPLICATION DATA:  
35 APPLICATION NUMBER: US/08/487,826H  
36 FILING DATE: 10-SEP-1993  
37 CLASSIFICATION: 435  
38  
39 ATTORNEY/AGENT INFORMATION:  
40 NAME: ISTRATISCO, Ned  
41 REGISTRATION NUMBER: 29,655  
42 REFERENCE/SEQUENCE NUMBER: NIH21-001CP1  
43 TELECOMMUNICATION: INTERNATIONAL:  
44 TELEPHONE: (619) 245 8050  
45 TELEFAX: (619) 245 0176  
46  
47 INFORMATION FOR SEQ. ID NO.: 13:  
48 SEQUENCE CHARACTERISTICS:  
49 LENGTH: 19124 base pairs  
50 TYPE: nucleic acid  
51 STRANDEDNESS: single





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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,658
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Salimchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UP114.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Amsacta moulai entomopoxvirus
FEATURE:
NAME/KEY: CDS
LOCATION: complement (18..218)
FEATURE:
NAME/KEY: CDS
LOCATION: complement (234..782)
FEATURE:
NAME/KEY: CDS
LOCATION: 852..1511
US-08-107-755A-8

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Query Match 5.4%; Score 52; DB 1; Length 1511;  
 Best Local Similarity 44.7%; Pred No 0.011;  
 Matches 298, Conservative 0; Mismatches 355, Indels 13, Gaps 2.

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OY 43 taaagtttagttagcaagtggtacatttatttgaaacaaatacaccactaac 102
   || || || || || || || || || || || || || || || || || || ||
DB 615 TAAATATTTTCGTCATGATTTATATTTTATTAATATATATATATATATG 674
OY 103 tgtataaacaatataaacaatagaagaaatagaatagaatagaatagaat 162
   || || || || || || || || || || || || || || || || || || ||
DB 675 AGTAAATACACATTTTTCATTAACATTAACATTAACATTAACATTAAC 734
OY 163 tgaatattgaacaacatttttgaacacattga-----gaatatttgaac 213
   || || || || || || || || || || || || || || || || || || ||
DB 735 TGTGTTTTCGACGAGAACATAGACCATATATATATATATATATATATAT 794
OY 214 tctcttctgctgctgaacacacacacacacacacacacacacacacacac 273
   || || || || || || || || || || || || || || || || || || ||
DB 795 TTTGATATATTTTTCACAAAAAATTAATCATGAAAAAATTAATATCATG 854
OY 274 aatgtgagatagaagagaagatgtgacaaagtgtacaaagtgtacaaagtgc 333
   || || || || || || || || || || || || || || || || || || ||
DB 855 GATTTACATAAATTCGATATTAATTAATTAATTAATTAATTAATTAATTA 914
OY 334 attgagaatttgacaaagtgcacaaagtgcacaaagtgcacaaagtgcac 393
   || || || || || || || || || || || || || || || || || || ||
DB 915 ATATATATTAACAGAGATATATATATATATATATATATATATATATAT 974
OY 394 gaccattagagaatgtgacattagaatatttgccagtcattgaacaaaga 453
   || || || || || || || || || || || || || || || || || || ||
DB 975 GAAGATTTGCATATATATATATATATATATATATATATATATATATAT 1034
OY 454 aatattttttaaataatattgaatcattgaatcattgaatcattgaatc 513
   || || || || || || || || || || || || || || || || || || ||
DB 1035 AAAAGTTATATATTTCAAAATTAATATATATATATATATATATATAT 1094

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OY 514 gatgaagagattggaatgaatgtgattgaattgaattggtgcgaattaa 573
   || || || || || || || || || || || || || || || || || || ||
DB 1095 AATATACATATTTTACATATATCTATTAACAAAAATAGCAATATTAAT 1154
OY 574 aatttgatatttctatataatgaagatgaatgaatgaatgaatgaatga 633
   || || || || || || || || || || || || || || || || || || ||
DB 1155 GCACATATCAATGAAATTTTAAATTCGATATATATATATATATATATAT 1210
OY 634 tagatcaataagagaataaacgatatataatccctcgaacaaacaaac 693
   || || || || || || || || || || || || || || || || || || ||
DB 1211 TATATATATTTTACATAATTTAAAAAATTAATATATATATATATAT 1270
OY 694 tactaa 699
   || || ||
DB 1271 TATATAA 1276

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RESULT 13  
 US-08-544-332-8  
 Sequence 8, Application US/08544332  
 Patent No. 5935777  
 GENERAL INFORMATION:  
 APPLICANT: Meyer, Richard W.  
 APPLICANT: Hall, Richard L.  
 APPLICANT: Guidi, Michael F.  
 TITLE OF INVENTION: NO. 5935777-1 Entomopoxvirus Expression System  
 NUMBER OF SEQUENCES: 77  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Gerard H. Hengen  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1 0, Version #1 25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/544,332  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/991,867  
 FILING DATE: 07-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/107,755  
 FILING DATE: 19-AUG-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO 92/14818  
 FILING DATE: 12-FEB-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/827,685  
 FILING DATE: 30-JAN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/657,584  
 FILING DATE: 19-FEB-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hengen, Gerard H.  
 REGISTRATION NUMBER: 35,746  
 REFERENCE/DOCKET NUMBER: UP114.C4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1511 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: unknown  
 MOLECULE TYPE: DNA (genomic)











[illegible][illegible]















[illegible]

RESULT 3  
 AAS02126  
 ID MAS02126 standard: DNA: 1350 bp  
 AC AAS02126;  
 XX  
 XX 18-JUL-2001 (first entry)  
 DT  
 DE Promoter #1 for regulating expression of foreign genes  
 XX  
 XX Promoter; transgenic plant; monocotyledon, dicotyledon, gymnosperm, ds.  
 KW Synthetic.  
 OS  
 XX WO200125455 A2.  
 FN  
 XX 12-APR-2001.  
 PD  
 XX 02-OCT-2000. 2000W017A01144  
 PF  
 XX 04-OCT-1999; 99QS-0157129  
 PR  
 XX (MEDI-) MENTICAGO INC.  
 PA  
 XX Vezina L, D'Aoust M;  
 PI  
 XX WPI: 2001-266316/27.  
 DR  
 XX Novel Promoter for regulating expression of foreign genes in transgenic  
 PT organisms, more specifically in a leaf-specific manner in transgenic  
 PT plants -  
 PT  
 XX Claim 1; Page 8; 9pp; English.  
 PS  
 XX The sequence represents the coding sequence of Promoter #1 for regulating  
 CC expression of foreign genes in transgenic organisms. The promoter is  
 CC useful for regulating the expression of foreign genes in transgenic  
 CC organisms, particularly plants, e.g., monocotyledons, dicotyledons or  
 CC gymnosperms, by preparing a transgenic organism using an expression  
 CC construct comprising the promoter and an open reading frame (ORF) of a  
 CC gene.  
 CC  
 XX Sequence 1350 BP; 482 A; 236 C; 230 G; 402 T, 0 other.

Query Match	100.0%;	Score 731;	DB 22;	Length 1350;
Test local Similarity	100.0%;	Préd No	6	8G-133;

Matches 731; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Accession	Source	Length (bp)	Insertion Site	Notes
AA096458	AA096458	623	BP.	Standard DNA
XX	AA096458			
AC	AA096458			
XX				
DT	08-FEB-2001			(first entry)
XX				
DE	Nucleotide sequence of the promoter MPr1097.			
XX				
KM	pLp1 promoter; chlorotic promoter; transgenic plant; MPr1097			
KM	plastocyanin gene promoter; ss.			
XX				
OS	Synthetic.			
OS	Pisum sativum.			
XX				
PN	WO20050906-A1.			
XX				



XX petE promoter; chimeric promoter; transgenic plant; MPT1096;  
 KM plastocyanin gene promoter; ss.  
 XX Synthetic.  
 OS Pisum sativum.  
 XX WO200056906-A1.  
 XX 28-SEP-2000.  
 XX 20-MAR-2000; 2000WO-1R00317.  
 XX 22-MAR-1999; 99FR-0003635.  
 XX (MERI-) MERISTEM THERAPEUTICS.  
 PA Rance I, Gruber V, Theisen M.  
 PI Rance I, Gruber V, Theisen M.  
 DR WPI; 2000-587667/55.  
 XX Chimeric expression promoter for producing dicotyledonous and  
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence  
 PT derived from a promoter of the pea plastocyanin gene.  
 XX Claim 2; Page 67; 83pp; English.  
 XX The present sequence represents the chimeric promoter MPT1096. The  
 CC promoter is derived from the petE promoter from pea plastocyanin gene,  
 CC by a deletion in 5' of the repeated invert sequences of the as 1 like  
 CC and enhancer like elements borne by two SphI fragments of 403 bp. The  
 CC petE promoter directs cell-specific but not full light-regulated  
 CC expression in transgenic tobacco plants. The promoter is used to  
 CC construct chimeric promoters of the invention. The specification  
 CC describes a chimeric expression promoter comprising a promoter of the  
 CC pea plastocyanin gene, or comprising a G box operably or functionally  
 CC linked upstream of a CAAT box, TATA box and transcription initiation  
 CC site. The chimeric promoters are used in expression vectors for  
 CC producing transgenic plants, such as dicotyledonous species,  
 CC e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,  
 CC rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,  
 CC barley, oat, rice, or corn.  
 CC  
 CC Sequence 326 bp; 111 A; 91 C; 38 G; 86 T; 0 other;  
 SO

Query Match 25.9%; Score 189.6; DB 21; Length 325;  
 Best local Similarity 84.8%; Pred. No. 4, 1e-28;  
 Matches 224; Conservative 0; Mismatches 39; Indels 1; Gaps 1;

QY 448 tatatttaaaataaataaagccagtaagagataaataaataaataaataaataa 507  
 DB 39 tatataaaataaataaagccagtaagagataaataaataaataaataaataa 98  
 QY 508 caatccagtagataaataaataaagccagtaagagataaataaataaataaataa 567  
 DB 99 caatccagtagataaataaataaagccagtaagagataaataaataaataaataa 158  
 QY 568 aaatcaaatatcttcacacatcttagcaacaaataaataaataaataaataaataa 626  
 DB 159 aaatcaaatatcttcacacatcttagcaacaaataaataaataaataaataaataa 218  
 QY 627 caatccagtagataaataaataaagccagtaagagataaataaataaataaataa 686  
 DB 219 caatccagtagataaataaataaagccagtaagagataaataaataaataaataa 278  
 QY 687 aagagaagagataaataaataaataaataaataaataaataaataaataaataa 710  
 DB 279 aatccagtagataaataaataaataaataaataaataaataaataaataaataa 302

ID AAA96460 standard; DNA; 207 bp.  
 XX  
 AC AAA96460;  
 XX  
 DT 08-FEB 2001 (first entry)  
 XX  
 DE Nucleotide sequence of the promoter MPT1096.  
 XX  
 KM petE promoter; chimeric promoter; transgenic plant; MPT1097;  
 KM plastocyanin gene promoter; ss.  
 XX Synthetic.  
 OS Pisum sativum.  
 XX WO200056906-A1.  
 XX 28-SEP-2000.  
 XX 20-MAR-2000; 2000WO-1R00317.  
 XX 22-MAR-1999; 99FR-0003635.  
 XX (MERI-) MERISTEM THERAPEUTICS.  
 PA Rance I, Gruber V, Theisen M.  
 PI Rance I, Gruber V, Theisen M.  
 DR WPI; 2000-587667/55.  
 XX Chimeric expression promoter for producing dicotyledonous and  
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence  
 PT derived from a promoter of the pea plastocyanin gene.  
 XX Claim 2; Page 67; 83pp; English.  
 XX The present sequence represents the chimeric promoter MPT1098. The  
 CC promoter is derived from the petE promoter from pea plastocyanin gene,  
 CC and contains only the TATA and CAAT boxes, and corresponds to a  
 CC minimal reference promoter on the petE promoter. The petE promoter  
 CC directs cell-specific but not full light-regulated expression in  
 CC transgenic tobacco plants. The promoter is used to construct chimeric  
 CC promoters of the invention. The specification describes a chimeric  
 CC expression promoter comprising a promoter of the pea plastocyanin gene,  
 CC or comprising a G box operably or functionally linked upstream of a CAAT  
 CC box, TATA box and transcription initiation site. The chimeric promoters  
 CC are used in expression vectors for producing transgenic plants, such as  
 CC dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,  
 CC rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,  
 CC barley, oat, rice, or corn.  
 CC  
 CC Sequence 207 bp; 67 A; 58 C; 21 G; 61 T; 0 other;  
 SO

Query Match 15.9%; Score 116; DB 21; Length 207;  
 Best local Similarity 84.5%; Pred. No. 7, 1e-14;  
 Matches 142; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

QY 544 ctctgagacatcttaataaataaataaataaataaataaataaataaataaataa 603  
 DB 16 ctctgagacatcttaataaataaataaataaataaataaataaataaataaataa 75  
 QY 604 aaatcaaatatcttcacacatcttagcaacaaataaataaataaataaataaataa 662  
 DB 76 aaatcaaatatcttcacacatcttagcaacaaataaataaataaataaataaataa 145  
 QY 663 ctctgagacatcttaataaataaataaataaataaataaataaataaataaataa 710  
 DB 136 ctctgagacatcttaataaataaataaataaataaataaataaataaataaataa 183

[illegible]

XX	OR FRB 2001 (1178st cont'd)
DE	Nucleotide sequence of the promoter Mm1108
XX	
XX	pEF- <i>Chimie</i> : chimie promoter; *transgene for a <sup>+</sup> ; Mm1108
KW	plastocyanin gene promoter; ss
XX	Synthetic
OS	Plasmid vector.
FN	M200056906 A1
XX	
P0	28 SEP 2000.
FE	Z0 MAR 2000; Z000W [R06A17.
XX	
XX	Z0 MAR 1999; 99FR 0006645.
FR	(MIR) MERISM IREXAPPELUS.
PA	Rouze L., Grollet V., Theissen M.
E1	WPI: Z000 587661/15.
XX	
PT	chimie expression promoter for producing dicotyledonous and monocotyledonous transgenic plants comprises a nucleic acid sequence derived from a promoter of the pea plastocyanin gene
XX	claim 2; page 68; 8pp; English.
XX	
OC	The present sequence represents the chimie promoter Mpl10m. The promoter is derived from the pEF- <i>Chimie</i> promoter from pea plastocyanin gene, by fusing the pEF as 1 like and non enhancer like elements to the promoter Mpl10m (comprising TATA and CAAT boxes of pEF). The pEF- promoter directs cell specific but not full light regulated expression in transgenic tobacco plants. The promoter is used to construct chimie promoters of the invention. The specification describes a chimie expression promoter comprising a promoter of the pea plastocyanin gene, or comprising a G box operably or functionally linked upstream of a CAT box, LAT box and transcription initiation site. The chimie promoters are used in expression vectors for producing transgenic plants, such as dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.
CC	
XX	Sequence 281 BP; 95 A; 71 C; 45 G; 80 T; 6 other.
GC	
GC	Query Match 12.2% Score 89.4; 98 % length 281
GC	Fast Local Similarity 77.8%; Prod No. 10 000
GC	Matches 145; Conserved size 0; Mismatches 46; Indels 2; Gaps 2
GC	
GC	5'1 GGCTGCTGTGGTGTGAATATCAAGCATTCAGCAGATTTACAGAGTAAGCGG
GC	TTTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT
GC	88 GAAGATCTTGAGATCAATTATCAATCAAAATATCTCTGATGATGATGATGATG
GC	GGT
GC	681 CAAAACAAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG
GC	TTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT
GC	147 CAAAAACCAAGCAAGATCAATGATGATGATGATGATGATGATGATGATGATGATG
GC	GAT
GC	660 CACTTATGCTTCAGAGCAATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
GC	TTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT
GC	10b 207 TCTTGGATCTCTCAAGATCAATGATGATGATGATGATGATGATGATGATGATG
GC	AT
GC	HESEU1
GC	AAA96463
ID	AAA96463 standard; INNA; 280 BP.
XX	AAA96463;
AC	
XX	OR FRB 2001 (1178st cont'd)



RESULT 12

AAAG6464

ID AAAG6464 standard: INA 600 bp

XX AAAG6464:

XX 08 FEB 2001 (first entry)

DE Nucleotide sequence of the promoter MP1154

XX potE promoter; chimeric promoter; Transgenic plant: MP1154

XX plastocyanin gene promoter; ss.

XX Synbiolec

XX Pisum sativum

XX W6200056906.A1

XX 28 SEP 2000

XX 20 MAR 2000; 2000W61800417

XX 22 MAR 1999; 99PR 0006645

XX (MER1) MERISTEM THERAPEUTICS

XX Ranee L, Grubbs V, Thelsson M

XX MP1: 2000 587667/55

chimeric expression promoter for producing monoclonal and monoclonal Transgenic plants comprises a nucleic acid sequence derived from a promoter of the pea plastocyanin gene

claim 2: Page 71: 8 (pp): English

The present sequence represents the chimeric promoter MP1153. The promoter is derived from the potE promoter from pea plastocyanin gene. The potE promoter directs cell specific but not full light regulated expression in transgenic tobacco plants. The promoter is used to construct chimeric promoters of the invention. The specification describes a chimeric expression promoter comprising a promoter of the pea plastocyanin gene, or comprising a 6 box operably or functionally linked upstream of a CAAT box, TATA box and transcription initiation site. The chimeric promoters are used in expression vectors for producing transgenic plants, such as monoclonal species, e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower, and monoclonal species, e.g. wheat, barley, oat, rice, or corn.

Sequence 603 bp; 101 A 76 C 41 G 83 T 0 other

Query Match 12.3% Score 89; DB 21; Length 405

Best Local Similarity 76.2% Prod. No. 1.2e-08

Matches 144; Conservative 7; Mismatches 25; Indels 29; Gaps 2

542 exact match of a nucleotide

91 exact match of a nucleotide

504 exact match of a nucleotide

143 exact match of a nucleotide

642 exact match of a nucleotide

211 exact match of a nucleotide

702 exact match of a nucleotide

271 exact match of a nucleotide

271 exact match of a nucleotide

271 exact match of a nucleotide

RESULT 13

AAAG6466

ID AAAG6466 standard: INA 270 bp

XX AAAG6466:

XX 08 FEB 2001 (first entry)

DE Nucleotide sequence of the promoter MP1145

XX potE promoter; chimeric promoter; Transgenic plant: MP1145

XX plastocyanin gene promoter; ss.

XX Synbiolec

XX Pisum sativum

XX W6200056906.A1

XX 28 SEP 2000

XX 20 MAR 2000; 2000W61800417

XX 22 MAR 1999; 99PR 0006645

XX (MER1) MERISTEM THERAPEUTICS

XX Ranee L, Grubbs V, Thelsson M

XX MP1: 2000 587667/55

chimeric expression promoter for producing monoclonal and monoclonal Transgenic plants comprises a nucleic acid sequence derived from a promoter of the pea plastocyanin gene

claim 2: Page 72: 8 (pp): English

The present sequence represents the chimeric promoter MP1144. The promoter is derived from the potE promoter from pea plastocyanin gene, by fusing the potE as 1 like and was behavior like elements to the promoter MP1098 (comprising TATA and CAAT boxes of potE), and then inserting a G box and fusing a fragment comprising a duplication of the element as2 and as1. A 72 bp fragment comprising the elements as 2, as 1 and as 1 was then deleted. The potE promoter directs cell specific but not full light regulated expression in transgenic tobacco plants. The promoter is used to construct chimeric promoters of the invention. The specification describes a chimeric expression promoter comprising a promoter of the pea plastocyanin gene, or comprising a 7 box operably or functionally linked upstream of a CAAT box, TATA box and transcription initiation site. The chimeric promoters are used in expression vectors for producing transgenic plants, such as monoclonal species, e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower, and monoclonal species, e.g. wheat, barley, oat, rice, or corn.

Sequence 220 bp; 73 A 60 C 26 G 61 T 0 other

Query Match 12.3% Score 88.4; DB 21; Length 220

Best Local Similarity 81.0% Prod. No. 1.4e-08

Matches 115; Conservative 07; Mismatches 28; Indels 1; Gaps 12

570 exact match of a nucleotide

55 exact match of a nucleotide

642 exact match of a nucleotide

115 exact match of a nucleotide

584 exact match of a nucleotide

171 exact match of a nucleotide

171 exact match of a nucleotide

171 exact match of a nucleotide



Tue Sep 3 13:59:10 2002

us-09-678-303-3.rng

Page 10

Search completed: Sep 03 01:04:22  
Job: 1 time: 8074 secs

[illegible]

BASE COUNT	170	147	119	174	others
ORIGIN					

Matches: 112; Conserved: 0; Mismatches: 6; Gaps: 1.

[illegible]

61 TTTGTAATTATTTTTAAATAAAGGAAGAATAAACCTTAAATAC

121 A 121

## ESQIT 2

№047A021F' 6', МРНА -нејасно

### III. E

Kosidae; Kosiidae; Labellidae; Labellulidae; Papilionoidae; Tridolidae;

FLORES, H. R., [unnamed], J. A. WELTER, J. W., and MAY, D. D.

CONTACT: May 10

2510 Sam Noble Parkway,  
Atmore, OK 74402, USA  
Tel.: 580 221 7391

Insert length: 604      tested filter: 0.00  
plateau: 0.04      rows: 102

## Source

"Realizing that the only way to develop the

Young, active, pioneering, mature and sophisticated leaders."

Query Match	11.78: Score 85.8; Dis 13; Length 684
11.78: Score 85.8; Dis 13; Length 684	11.78: Score 85.8; Dis 13; Length 684

Y. G. (1994) *Journal of the American Statistical Association* 89, 1047-1054.

[illegible]

802 P 802. A

DEFINITION	NO.10560/PLP1054	phosphate-stimulated leaf modification of RNA
NO.05	1054	1054
NO.03	1054	1054
NO.02	1054	1054
NO.01	1054	1054

ERSLON 13645/5th 11 0111480804  
EYMORE'S FST

REFERENCE  
1. (bases 1 to 637)  
AUTHORS  
Harris A B  
Scott A D  
Goulden H A  
Holmes I J

Medicago truncatula phosphate-starved leaf library

# The Samuel Roberts Not

Enid I.: mjharrison@noble.com

### Location/Qualifiers

[illegible]

Vector: Lambda Zap; At the

period, the plants were fertilized twice weekly with 1/2 Hoagland solution containing 200M potassium

Hest Local Similarity = .91; Pred. No. = 0.0001?;

[illegible]

FEATURES	SEQUENCE
REFERENCE	
1. (bases 1 to 483)	
2. Flores, H.R., Imman, J.T., Moller, J.W. and May, G.D.	
3. Expressed Sequence Tags from the Samuel Roberts Noble Foundation	
4. Medicago truncatula leaf library	
5. Unpublished (2000)	
6. on Jul 13, 2000. This sequence version replaced GI:9119461.	
7. Contact: May, G.D.	
8. Plant Biology Division	
9. The Samuel Roberts Noble Foundation	
10. 2510 Sam Noble Parkway, Ardmore, OK 73402, USA	
11. Tel: 580 221 7391	
12. Fax: 580 221 7380	
13. Email: gdmay@noble.org	
14. Medicago Genome Initiative accession: MG15014974	
15. Insert length: 671	
16. Std Error: 0.00	
17. Plate: 014	
18. Row: 6	
19. Column: 06	
20. Seq primer: TCACACAGGAACACACATGAC.	
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22. 1..483	
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24. /db_xref="taxon:3880"	
25. /clone="NP014F061.P"	
26. /note="Developing leaf"	
27. /tissue_type="leaf"	

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Location/Qualifiers
1.483
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="Nr014P061.p"
/version_id="Developing leaf"
/tissue_type="leaf"
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	LOCUS	CNS002JL	1101 bp	DNA	linear	GSS 03-JUN-1998
	DEFINITION	Drosophila melanogaster genome survey sequence; first end of BAC # BARO6N11 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
	ACCESSION	AL061936				
	VERSION	ALI061936..1	GI:4940214			
	KEYWORDS	GSS.				
	SOURCE	fruit fly.				
	ORGANISM	Drosophila melanogaster				
	AUTHORS	Eukaryota, Metazoa, Arthropoda, Tracheata, Insecta;				
	TITLE	Pterygota, Neoptera, Endopterygota, Diptera, Brachycera;				
	JOURNAL	Muscomorpha, Ephydroidea; Drosophilidae, Drosophila. 1 (bases 1 to 1101)				
	COMMENT	Direct Submission Submitted (02-jun-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqet@genoscope.cns.fr)  Web : www.genoscope.cns.fr ) determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using three BACs. For further information please see http://www.fruitfly.org. The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Ito Osugawa and Aaron Mamosser in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI 98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the JIGS from the isogenic strain y2; cn bw sp, the same strain used for the BDGPs p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the HACBAC Resource Center can be found at http://arapac.med.buffalo.edu/drosophila_bac.htm.  Location/Qualifiers 1..1101 /organism="Drosophila melanogaster" /db_xref=taxon:7227 /clone_lib="RPCI-98" /clone="BARC05N11" /note="end : TET3"				
	FEATURES					
	source					
	BASE COUNT	631 a      7 c      28 g      289 t      146 others				
	ORIGIN					
OY	Query Match	9.8%; Score 72; DB 12; Length 1101:				
	Best Local Similarity	43.6%; Pred. NO. 0.02:				
	Matches 198; Conservativa	21; Mismatches 235; Indels 0; Gaps 0;				
DB	1 agaggaagaaggaaaggggagatataaaaactaatgtgatgatgagagaagtctta 60					
	AAAAAAAAAAAAA					
OY	61 caaaqtlqlaccacaatlqtlcaaatcatcattlqqaalqttaaqaqcatacca 120					
DB	318 CAAAATAAAATTTTCTTAATTGTGGTGAGCGTCCTCAATGAAGAAGTCCGC 377					
	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA					
OY	121 aaataagqatlaalgcyltaataataaqatgacgccattlaagaagaatqlacca 180					
	" " " " " "					
DB	378 AAAAAAATAAACATCATATTTCTTATTTTCTTATTTCTTATTTCTTATTTCTT 437					
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OY	181 gaatttcggcaagccatcaaagaagaataattttttaaadtaaacgtcgatt 240					
	" " " " " "					
DB	438 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 497					
	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA					
OY	241 calligaltaaacatlgalltattlaattaatgaaatgataaagatttgatat 300					
	" " " " " "					
DB	498 AAAAAAANAANAATAATTAATTTTCTTATTTCTTATTTCTTATTTCTTATTTCTT 557					
	AAAAAAAAAAAAAAAAATAATTAATTTTCTTATTTCTTATTTCTTATTTCTTATTTCTT					
OY	301 laigiaatlaaatltggucgiccatattiaattgcaattlgaatclittcataata 360					
	:             :					
DB	558 TWTTATATTTTTATTTTTTAAMMAAATTTTAATAAANKAWMTWTNTTTTAAWTA 617					
OY	361 ccataagagtcacitaaactatttatataattcacatagataaataagaagaataacgtag 420					

1b 618 AAAAAATTTTAAANAWTTTTTTTTTTTAAITAAIAAAAAAANAAIAAAAWITWITA 677  
 Qy 421 attaatccctccataaaaaaaacgatattt 454  
 Db 678 TTTAATTAAATTTAAATTTTAAAAAWTTTTTTTAAWT 711

Search completed: August 31, 2009, 23:46:55  
Job time: 19101 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: September 2, 2002, 00:57:51 : Search time 96.05 seconds  
(without alignments)  
1869.423 Million cell updates/sec

Title: US-09-678-303-3

Perfect score: 731

Sequence: 1 agagagaagaagaagaag 731

Scoring table: IDENTITY NUC Gapout 1 0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:

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4: /cgn2\_6/pdata/1/ina/6B.COMB.seq:\*

5: /cgn2\_6/pdata/1/ina/6C.COMB.seq:\*

6: /cgn2\_6/pdata/1/ina/6D.COMB.seq:\*

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20: /cgn2\_6/pdata/1/ina/6R.COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	61	8.3	7218	1	Sequence 14, App1
2	48	6.6	2317	3	Sequence 5, App1
3	48	6.6	3974	4	Sequence 3, App1
4	47.4	6.3	837	4	Sequence 288, App1
5	46	6.3	19124	2	Sequence 13, App1
6	45.8	6.3	5852	1	Sequence 2, App1
7	45.4	6.2	6768	1	Sequence 1, App1
8	45.4	6.2	8457	2	Sequence 1, App1
9	45.4	6.2	8457	2	Sequence 1, App1
10	45	6.2	19124	2	Sequence 13, App1
11	44.8	6.1	847	4	Sequence 288, App1
12	44.6	6.1	2251	4	Sequence 3, App1
13	44.6	6.1	3095	6	Sequence 13, App1
14	44.4	6.1	615	4	Sequence 2, App1
15	44.2	6.0	8920	2	Sequence 1, App1
16	44.2	6.0	8920	2	Sequence 1, App1
17	43.6	6.0	3350	4	Sequence 3, App1
18	43.4	5.9	740	4	Sequence 288, App1
19	43.4	5.9	6243	2	Sequence 13, App1
20	42.8	5.9	8920	4	Sequence 2, App1
21	42.8	5.9	8920	4	Sequence 2, App1
22	42.2	5.8	15231	3	Sequence 1, App1
23	42.2	5.8	176373	3	Sequence 1, App1
24	42	5.7	863	4	Sequence 288, App1
25	41.8	5.7	3618	1	Sequence 1, App1
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27	41.6	5.7	7653	3	Sequence 1, App1

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33	41	5.6	8457	4	Sequence 1, App1
34	41	5.6	1450	3	Sequence 1, App1
35	40.8	5.6	5852	1	Sequence 2, App1
36	40.8	5.6	5852	1	Sequence 2, App1
37	40.6	5.6	662	4	Sequence 1, App1
38	40.6	5.6	662	4	Sequence 1, App1
39	40.6	5.6	662	4	Sequence 1, App1
40	40.6	5.6	701	4	Sequence 1, App1
41	40.6	5.6	711	4	Sequence 1, App1
42	40.6	5.6	724	4	Sequence 1, App1
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44	40.6	5.6	767	4	Sequence 1, App1
45	40.6	5.6	827	4	Sequence 1, App1

## ALIGNMENTS

RESULT 1  
US-08-232-463-14/C  
Sequence 14, Application US/0822463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEFFLINGER, F.  
TITLE OF INVENTION: PERMANENT FOWLEPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESS: Policy & Partner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-08-232-463  
FILING DATE:  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08-232-463  
FILING DATE:  
APPLICATION NUMBER: 08-232-463  
FILING DATE: 08-23-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
PREPARATION NUMBER: 29,768  
REFERENCE/DEPT NUMBER: 38472, 114 1MMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)836-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZ19-C-F15  
US-08-232-463-14

15: 08 749 522 5

[illegible]





1 CURRENT APPLICATION DATA:  
2 APPLICATION NUMBER: US/08/107,755A  
3 FILING DATE: 19-AUG-1993  
4 CLASSIFICATION: 435  
5 PRIOR APPLICATION DATA:  
6 APPLICATION NUMBER: US 07/827,658  
7 FILING DATE: 30-JAN-1992  
8 PRIOR APPLICATION DATA:  
9 APPLICATION NUMBER: US 07/657,584  
10 FILING DATE: 19-FEB-1991  
11 ATTORNEY/AGENT INFORMATION:  
12 NAME: Saliwanichik, David R.  
13 REGISTRATION NUMBER: 31,794  
14 REFERENCE/DOCKET NUMBER: UFI14.C2  
15 TELECOMMUNICATION INFORMATION:  
16 TELEPHONE: (904) 375-8100  
17 TELEFAX: (904) 372-5800  
18 INFORMATION FOR SEQ ID NO: 1:  
19 SEQUENCE CHARACTERISTICS:  
20 LENGTH: 6768 base pairs  
21 TYPE: nucleic acid  
22 STRANDEDNESS: double  
23 TOPOLOGY: unknown  
24 MOLECULE TYPE: DNA (genomic)  
25 ORIGINAL SOURCE:  
26 ORGANISM: Amsacta moorei entomopoxvirus  
27 FEATURE:  
28 NAME/KEY: CDS  
29 LOCATION: complement (65..1459)  
30 FEATURE:  
31 NAME/KEY: CDS  
32 LOCATION: 1474..2151  
33 FEATURE:  
34 NAME/KEY: CDS  
35 LOCATION: complement (2475..2475)  
36 FEATURE:  
37 NAME/KEY: CDS  
38 LOCATION: 2502..2987  
39 FEATURE:  
40 NAME/KEY: CDS  
41 LOCATION: 3080..6091  
42 FEATURE:  
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44 LOCATION: complement (6277..6768)  
45 US-(8-107-755A-1

Query Match 6.2%; Score 45.4; DH 1; Length 6768;  
Best Local Similarity 48.3%; Pred. No. 0.14;  
Matches 156, Conservative 0; Mismatches 166; Indels 1; Gaps 1;  
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DB 2135 AAAAGTCTTCTACCTGATTAATTAATAAATGATATTATACAGTTATTTATCTAAT 2076  
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DB 2075 CTCACATTAGTAAATACCAAAATTTAATATATTAATTAATAGATATATATTATTT 2016  
QY 348 cctatatatgcccataagatgtaactatttataatttcaatgaagaataaga 407  
DB 2015 AGGGGATTTCTCTATTAATTACATATTTATATCTAGATTTCATTAATCTTAATGT 1956  
QY 408 gaataacgatatataatccct 430  
||| ||| ||| |||

DB 1955 GATACATATCTAATACATCACT 1933  
RESULT 8  
US-07-991-867B-1/c  
Sequence 1, Application US/07991867B  
Patent No. 5476781  
GENERAL INFORMATION:  
APPLICANT: Meyer, Richard W.  
APPLICANT: Hall, Richard L.  
APPLICANT: Grudl, Michael E.  
TITLE OF INVENTION: No. 5476781c1 Entomopoxvirus Expression System  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanichik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/991,867B  
FILING DATE: 12-DEC-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 92/14818  
FILING DATE: 12-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,685  
FILING DATE: 30-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/657,584  
FILING DATE: 19-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanichik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: UFI14.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8457 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Amsacta moorei entomopoxvirus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: complement (65..1459)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1474..2151  
FEATURE:  
NAME/KEY: CDS  
LOCATION: complement (2475..2475)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2502..2987  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3080..6091  
FEATURE:  
NAME/KEY: CDS  
LOCATION: complement (6277..6768)  
US-07-991-867B-1

100

100

RESULT 10  
US-08-487-8268-13/C  
Sequence 13, Application 03/084878268  
Patent No. 5993827  
GENERAL INFORMATION:  
APPLICANT: Sim, Kim L.  
APPLICANT: Chinisin, Chelan  
APPLICANT: Miller, Louis H.





STRANDEDNESS: single

Search completed. September 1, 2002, 00:58:27  
Job time: 7979 sec



pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARY

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No.	Score	Match	Length	PR	ID
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					Description

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2	971	71.9	921	6	AX105268	AX105268	Sequence
3	731	51.1	731	6	AX105269	AX105269	Sequence
4	57	4.2	526	6	AX036597	AX036597	Sequence
5	57	4.2	623	6	AX036596	AX036596	Sequence
6	57	4.2	938	6	AX036595	AX036595	Sequence
7	57	4.2	894	6	PSPETP	XX813 P.sativum p	
8	57	4.2	1505	8	LEPLAS	X16082 fca gene 10	
9	34	2.5	68	6	AX036607	AX036607	Sequence
10	34	2.5	670	6	AX036600	AX036600	Sequence
11	32	2.4	207	6	AX036598	AX036598	Sequence
12	31	2.3	280	6	AX036601	AX036601	Sequence
13	31	2.2	306	6	AX036603	AX036603	Sequence
14	31	2.2	303	6	AX036602	AX036602	Sequence
15	27	2.0	72	6	AX036609	AX036609	Sequence
16	27	2.0	266	6	AC2982	AC2982	Sequence
17	25	1.9	220	6	AX036604	AX036604	Sequence
18	25	1.9	229	6	AX036616	AX036616	Sequence
19	25	1.9	216	8	ALFFHYT	ALFFHYT	Sequence
20	25	1.9	1215	8	MSU18296	MSU18296	Methicillin sa
21	24	1.8	1084	4	AB031455	AB031455	Medicocara
22	24	1.8	66957	9	AC080379	AC080379	Sequence
23	24	1.8	165618	40	AC074469	AC074469	Homo sapi
24	24	1.8	165918	9	AC104185	AC104185	Homo sapi
25	24	1.8	166381	39	AC021208	AC021208	Homo sapi
26	24	1.8	167918	2	AC104188	AC104188	Homo sapi
27	24	1.8	218126	2	AC1627083	AC1627083	Mus muscu
28	23	1.7	281	6	AX036599	AX036599	Sequence
29	23	1.7	5239	6	AX045124	AX045124	Sequence
30	23	1.7	7577	3	AE003225	AE003225	Sequence
31	23	1.7	38666	6	SPAC2409	SPAC2409	Sequence
32	23	1.7	134199	1	SYNLEFE	SYNLEFE	Sequence
33	23	1.7	265985	1	AC087226	AC087226	Mus muscu
34	23	1.7	349980	6	AX044557	AX044557	Sequence
35	23	1.6	1322	8	AX028202	AX028202	Sequence
36	22	1.6	33751	6	AC090966	AC090966	Mus muscu
37	22	1.6	93586	6	AL590487	AL590487	Human DNA
38	22	1.6	117541	2	AC104285	AC104285	Human DNA
39	22	1.6	130893	8	AC104711	AC104711	Orfyz sat
40	22	1.6	139423	8	AC080545	AC080545	Orfyz sat
41	22	1.6	149931	2	AC092243	AC092243	Human sapi
42	22	1.6	150030	9	AL157992	AL157992	Human DNA
43	22	1.6	160040	9	AL159152	AL159152	Human DNA
44	22	1.6	161927	2	AC084818	AC084818	Orfyz sat
45	22	1.6	167491	2	AC093442	AC093442	Orfyz sat

## ALIGNMENTS

RESULT	1
AXI05267	
LOCUS	AXI05267
DEFINITION	Sequence 1 from Patent WO0125455.
ACCESSION	AXI05267
VERSION	AXI05267.1 GI:13921417
KEYWORDS	
SOURCE	synthetic construct.
ORGANISM	synthetic construct. artificial sequence. 1 (bases 1 to 1350)
REFERENCE	Vezina,L.P. and D'Aoust,M.A. Promoter for regulating expression of foreign genes Patent: WO 0125455-A 1 12-Apr-2001; Medicago Inc. (CA)
AUTHORS	
TITLE	Localize/Qualifiers
JOURNAL	1. 1350 /organism="Synthetic construct" /db_xref="taxon:12630" /note="sequence to be used as a promoter for regulating expression"
FEATURES	
SOURCE	
BASE COUNT	482 a 482 c 430 g 402 t
ORIGIN	

[illegible][illegible]

	/note="Sequence to be used as a Promoter for regulating expression"		
BASE COUNT	299 a	113 c	109 g 210 t

[illegible]

RESULT	4			
AX036597	AX036597	326 bp	DNA	linear
LOCUS	AX036597			
DEFINITION	Sequence	3 from Patent FR2791358.		
ACCESSION	AX036597			
VERSION	AX036597.1	GI:1125192		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
JOURNAL				



misc\_feature 857..870  
 /note="box 1: homology"  
 TATA\_signal 903..910  
 mRNA 940..998  
 /gene="petE"  
 /product="plastocyanin"  
 gene 940..998  
 /gene="petE"  
 CDS 993..998  
 /gene="petE"  
 /codon\_start=1  
 /product="plastocyanin"  
 /protein\_id="CAA48393.1"  
 /db\_xref="GI:4379383"  
 /translation="MA"  
 BASIS COUNT 339 a 201 c 154 g 304 t  
 ORIGIN

Query Match 4.2%; Score 57; DB 8; Length 998;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-18;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 767 agataaccacttaagccagcactctgtgacatcatatataatcaaca 823  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 788 ACATACCACTTAAAGCCACGACCTCTGTGACATTAATTAATCAACA 844

RESULT 8  
 PSPIAS 1505 bp DNA linear PIN 27-MAR-1995  
 DEF NITION pea gene for plastocyanin.  
 ACCESSION X16082  
 VERSION X16082.1 GI:20845  
 KEYWORDS electron carrier; photosynthesis; plastocyanin.  
 SOURCE pea  
 ORGANISM Pisum sativum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciales;  
 Pisum.  
 REFERENCE 1 (bases 1 to 1505)  
 AUTHORS Last,D.L. and Gray,J.C.  
 TITILE plastocyanin is encoded by a single-copy gene in the pea haploid  
 genome  
 JOURNAL Plant Mol. Biol. 12, 655-666 (1989)  
 FEATURES  
 source Location/Qualifiers  
 1..1505  
 /organism="Pisum sativum"  
 /strain="keltham first"  
 /db\_xref="taxon:3888"  
 /clone="lambda-GPC3"  
 /issue\_type="Shools"  
 /clone\_lib="lambda FMBL3"  
 1..46  
 /note="imperfect direct repeat 1"  
 21..50  
 /note="imperfect direct repeat 2"  
 25..62  
 /note="imperfect direct repeat 3"  
 39..41  
 /note="aca was aga in []"  
 /citation=[1]  
 59..88  
 /note="imperfect direct repeat 2"  
 94..139  
 /note="imperfect direct repeat 1"  
 114..142  
 /note="imperfect direct repeat 2"  
 130..159  
 /note="imperfect direct repeat 2"  
 134..171  
 /note="imperfect direct repeat 3"

promoter 723..730  
 /note="pot. TATA box"  
 misc\_feature 758..761  
 /note="put. transcriptional start site"  
 CDS 813..1319  
 /note="precursor peptide (AA 69 to 99)"  
 /codon\_start=1  
 /protein\_id="CAA34212.1"  
 /db\_xref="GI:20846"  
 /db\_xref="SMIS-PROT:P16002"  
 /translation="MATVSTVAIPSPSLKTNAAIKVSAAMKIPSTSQSPPIQV  
 ASLKDPGVAVATAASAVIASNALAVAGASUGGLAVPSSELEVSAGIIVFKKNA  
 CPHNVVPEDEIDIPAGVIDASKISMEHEDLINAGEIVSYKIDAKGIYKFCQSHUQAG  
 MCGQVTVN"  
 BASIS COUNT 460 a 299 c 283 g 45 t  
 ORIGIN

Query Match 4.2%; Score 57; DB 8; Length 1505;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-18;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 767 agataaccacttaagccagcactctgtgacatcatatataatcaaca 823  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 608 ACATACCACTTAAAGCCACGACCTCTGTGACATTAATTAATCAACA 664

RESULT 9  
 AX036607 68 bp DNA linear PAT 16-NOV-2000  
 DEFINITION Sequence 13 from Patent FR2791358.  
 ACCESSION AX036607  
 VERSION AX036607.1 GI:11256202  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE 1 (bases 1 to 68)  
 AUTHORS Rance,I., Theissen,M. and Gruber,V.  
 JOURNAL Patent: FR 2791358-A 13-29-SEP-2000;  
 MERISTEM THERAPEUTICS (FR)  
 FEATURES  
 source Location/Qualifiers  
 1..68  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Directional building block S3-Directional building  
 block oligonucleotide for the construction of promoters by  
 1b-PCR"

BASIS COUNT 22 a 19 c 5 g 22 t  
 ORIGIN

Query Match 2.5%; Score 34; DB 5; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 790 cactctgtgacatcatatataatcaaca 823  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 12 CACTCTGTGACACATTAATTAATCAACA 45

RESULT 10  
 AX036600 250 bp DNA linear PAT 16-NOV-2000  
 DEFINITION Sequence 6 from Patent FR2791358.  
 ACCESSION AX036600  
 VERSION AX036600.1 GI:11256195  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE 1 (bases 1 to 250)  
 AUTHORS Rance,I., Theissen,M. and Gruber,V.  
 JOURNAL Patent: FR 2791358-A 13-29-SEP-2000;  
 MERISTEM THERAPEUTICS (FR)  
 FEATURES  
 source Location/Qualifiers  
 1..250  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Directional building block S3-Directional building  
 block oligonucleotide for the construction of promoters by  
 1b-PCR"



REFERENCE 1 (bases 1 to 303)  
 AUTHORS Rance, I., Theisen M. and Gruber, V.  
 JOURNAL Patent: FR 2791358-A 8 29-SEP-2000;  
 MERISTEM THERAPEUTICS (FR)

FEATURES  
 source  
 1..303  
 Location/Qualifiers  
 /organism="synthetic construct"

promoter  
 1..303  
 /note="The promoter Mp1153 was obtained by fusing a  
 sequence of 78 bp of the promoter pelc, stretching from  
 position -582 to position -510 bp modified by ad. junction  
 of a 'G' box  
 Promoter Mp1153"

BASE COUNT 101 a 78 c 41 g 83 t  
 ORIGIN

Query Match 2.3%; Score 31; DB 6; Length 303;  
 Best Local Similarity 100.0%; Proc. No. 0.00018;  
 Matches 31, Conservative 0, Mismatches 0; Indels 0; Gaps 0;

QY 790 cactctgtgacacatcattatctaatc 820  
 |||  
 Db 91 cactctgtgacacatcattatctaatc 121

RESULT 15  
 AX036609

LOCUS AX036609 72 bp RNA Linear FAT 16-NOV-2000  
 DEFINITION Sequence 15 from Patent FR2791358.  
 ACCESSION AX036609  
 VERSION AX036609.1 GI:11226204

KEYWORDS  
 SOURCE synthetic construct.

ORGANISM  
 synthetic construct.  
 artificial sequence.

REFERENCE 1 (bases 1 to 72)  
 AUTHORS Rance, I., Theisen M. and Gruber, V.  
 JOURNAL Patent: FR 2791358-A 15 29-SEP-2000;  
 MERISTEM THERAPEUTICS (FR)

FEATURES  
 source  
 1..72  
 Location/Qualifiers

/organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="directional building block S5-directional building  
 block oligonucleotide for the construction of promoters by  
 Id-PCR"

BASE COUNT 22 a 20 c 10 g 20 t  
 ORIGIN

Query Match 2.0%; Score 27; DB 6; Length 72;  
 Best Local Similarity 100.0%; Proc. No. 0.023;

Matches 27, Conservative 0, Mismatches 0; Indels 0; Gaps 0;

QY 794 ctgtgacacatcattatctaatc 820  
 |||  
 Db 1 ctgtgacacatcattatctaatc 27

Search completed: September 1, 2002, 03:06:49  
 Job time: 12046 sec

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text suggests that organizations should implement robust systems to track income, expenses, and assets, ensuring that all data is up-to-date and easily accessible.

2. The second part of the document addresses the challenges of data management in a digital age. It highlights the risks associated with data breaches and the loss of sensitive information. To mitigate these risks, the document recommends the use of secure storage solutions and the implementation of strict access controls. It also stresses the importance of regular data backups and the use of encryption techniques to protect data from unauthorized access.

3. The third part of the document focuses on the role of technology in improving operational efficiency. It discusses how automation can streamline repetitive tasks, reduce human error, and free up resources for more strategic activities. The text mentions various software tools and platforms that can be used to manage workflows, collaborate with team members, and analyze data in real-time. It encourages organizations to embrace digital transformation and invest in the necessary infrastructure to support these efforts.

4. The fourth part of the document explores the importance of continuous learning and development for the workforce. It argues that in a rapidly changing environment, employees must stay updated with the latest skills and knowledge to remain competitive. The document suggests that organizations should provide opportunities for training, workshops, and conferences. It also encourages a culture of learning where employees are encouraged to share their knowledge and experiences with colleagues.

5. The fifth part of the document discusses the importance of maintaining strong relationships with stakeholders. It emphasizes that effective communication is key to building trust and understanding. The text suggests that organizations should establish regular channels of communication with customers, suppliers, and other relevant parties. It also highlights the importance of listening to feedback and being responsive to the needs and concerns of stakeholders.

6. The sixth part of the document addresses the importance of maintaining a strong financial position. It discusses the need for careful budgeting and financial planning to ensure the long-term sustainability of the organization. The text suggests that organizations should monitor their financial performance closely and make adjustments as needed. It also emphasizes the importance of maintaining a healthy cash flow and managing debt effectively.

7. The seventh part of the document discusses the importance of maintaining a strong legal and regulatory framework. It emphasizes that organizations must comply with all applicable laws and regulations to avoid legal penalties and reputational damage. The text suggests that organizations should consult with legal counsel to ensure that their policies and procedures are compliant. It also highlights the importance of staying updated with changes in the legal and regulatory landscape.

8. The eighth part of the document discusses the importance of maintaining a strong environmental and social governance (ESG) profile. It emphasizes that organizations have a responsibility to the community and the environment. The text suggests that organizations should implement sustainable practices, such as reducing carbon footprint, conserving resources, and promoting social equality. It also encourages organizations to report on their ESG performance and engage with stakeholders on these issues.

9. The ninth part of the document discusses the importance of maintaining a strong corporate culture. It emphasizes that a positive and inclusive culture is essential for attracting and retaining top talent. The text suggests that organizations should define their core values and mission statement clearly. It also encourages organizations to foster a sense of belonging and pride among employees, and to encourage them to contribute to the organization's success.

10. The tenth part of the document discusses the importance of maintaining a strong reputation. It emphasizes that a good reputation is a valuable asset for any organization. The text suggests that organizations should monitor their reputation closely and respond promptly to any negative feedback or crises. It also encourages organizations to engage in corporate social responsibility (CSR) activities to enhance their reputation and build trust with the community.







[illegible]

## KRISHNAN

110	AAA064599 standard; 10M; 520 bp
XX	
A'	AAA064599
XX	
111	08 FEB 2001 (first entry)
XX	
112	Nucleotide sequence of the promoter
XX	
113	XX
XX	
114	poly (promoter) obtained from 10T; Transposon (plant); M171096
XX	
115	plastocyanin gene promoter; 18S
XX	
116	Synthetic
XX	
117	Plasmid salt form
XX	
118	XX
119	W0200056906 A1
XX	
120	28 SEP 2000
XX	
121	20 MAR 2000; 2000000 (b) seq.
XX	
122	22 MAR 1999; 99ER (00) seq.
XX	
123	(MER1 ) MERISTEM THERAPEUTIC
XX	
124	XXXX
125	XXXX
126	XXXX
127	XXXX
128	XXXX
129	XXXX
130	XXXX
131	XXXX
132	XXXX
133	XXXX
134	XXXX
135	XXXX
136	XXXX
137	XXXX
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291	XXXX
292	XXXX
293	XXXX
294	XXXX
295	XXXX
296	XXXX
297	XXXX
298	XXXX
299	XXXX
300	XXXX
301	XXXX
302	XXXX
303	XXXX
304	XXXX
305	XXXX

XX The present sequence represents the chimera promoter M2106. The  
 CC promoter is derived from the *pro* promoter from *pro* plastocyanin gene,  
 CC by a deletion in 5' of the repeated inverted sequences of the *pro* 1 like  
 CC and enhancer like elements borne by two Split Transforms of 400 bp. The  
 CC *pro* promoter directs very specific but not full *pro* regulated  
 CC expression in transgenic tobacco plants. The promoter is used to  
 CC construct chimera promoters of the invention. The specification  
 CC describes a chimera expression promoter comprising a product of the  
 CC *pro* plastocyanin gene, or comprising a *cat* box operably or functionally  
 CC linked upstream of a CAT box, EYFP box and transcription initiation  
 CC site. The chimera promoters are used in expression vectors for  
 CC producing transgenic plants, such as dicotyledonous species,  
 CC *pro*, *betula*, *tobacco*, *carotus*, *lactuca*, *tomato*, *nicotiana glauca*, *populus*,  
 CC *rapa*, *betula*, *populus*, *sunflower*, and monocotyledonous species, *zea mays*, *maiz*  
 CC barley, oat, rice, or corn.

五三二

	4.2M; Score 57; 16-21 length 569
Query Match:	100.0%; Pos. No. 4 to 15;
Best Local:	0; Mismatches 0; Indels 0; Gaps
Motif:	57; Conserved type
07	767 agatagccacattttaaaccacacattctgtagcattctcatctaacacaa gca                                                       10b 110 agataacccaacttaaacccaacacatttgtagcattctcatctaatccaa 166
XX	RESULT 5
XX	AAA96458 standard; 10NA; 624 bp.
XX	AAA96458;
XX	08 FEB-2001 (first entry)
XX	Nucleotide sequence of the promoter MP1097.
XX	polE promoter; chimeraic promoter; transgeneic plant; MP1097;
XX	plastocyanin gene promoter; ss
XX	Synthetic
XX	os
XX	pisum sativum
XX	w02c0056906_A1.
XX	28 SEP 2000.
XX	20 MAR 2000; 2000W04 1800417.
XX	22 MAR 1999; 99EP 0004645.
XX	(MORF) MERISTEM HERA(POL)1097.
XX	Randee T., Hubert V., Holston M.
XX	WP1: Z000 587667/55.
XX	chimeraic expression; promoter for production of proteins and
XX	molecularly produced transgeneic plants comprises a nucleic acid sequence
XX	derived from a promoter of the pea plastocyanin gene
XX	claim 2; para 66; 8pp; English.
XX	
XX	the present sequence represents the chimeraic promoter MP1097. The
XX	promoter is derived from the polE promoter from pea plastocyanin gene,
XX	by a deletion in 5' of the repeated invert sequences as well as the
XX	as a linker box borne on a SphI fragment of 412 bp. The polE promoter
XX	directs cell specific but not full light regulated expression in
XX	transgenic tobacco plants. The promoter is used to engineer other chimeraic
XX	promoters of the invention. The specification describes a chimeraic
XX	expression promoter comprising a promoter of the pea plastocyanin gene,
XX	

or comprising a G box operably or functionally linked upstream of a CAT box, TATA box and transcription initiation site. The chimeric promoters are used in expression vectors for producing transgenic plants, such as dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.

Sequence 623 BP; 230 A; 128 C; 82 G; 183 T; 0 other;

Query Match 4.2%; Score 57; DB 21; Length 623;

Best Local Similarity 100.0%; Pred. No. 3,2e-15; Mismatches 0; Indels 0; Gaps 0;

DB 767 agataaccacttaagccacgactctgtgacatcatcatcctcaatcaca 823  
407 agataaccacttaagccacgactctgtgacatcatcctcaatcaca 463

RESULT 6

AAA6457

ID AAA6457 standard; DNA; 834 BP.

XX AAA6457;

XX 08-FEB-2001 (first entry)

XX Nucleotide sequence of the pete promoter from plastocyanin gene

XX pete promoter; chimeric promoter; transgenic plant;

XX plastocyanin gene promoter; ss.

XX Pisum sativum.

XX WO200056906-A1.

XX 28-SEP-2000.

XX 20-MAR-2000; 2000WO-1B00317.

XX 22-MAR-1999; 99FR-0003635.

XX (MERI-) MERISTEM THERAPEUTICS.

XX Rance I, Gruber V, Theisen M;

XX WPI; 2000-587667/55.

XX Chimeric expression promoter for producing dicotyledonous and

XX monocotyledonous transgenic plants comprises a nucleic acid sequence

XX derived from a promoter of the pea plastocyanin gene

XX Claim 1; Page 65; 83pp; English.

XX The present sequence represents the pete promoter from the pea  
XX plastocyanin gene. The promoter directs cell-specific but not full  
XX light-regulated expression in transgenic tobacco plants. The promoter  
XX is used to construct chimeric promoters of the invention. The  
XX specification describes a chimeric expression promoter comprising a  
XX promoter of the pea plastocyanin gene, or comprising a G box operably  
XX or functionally linked upstream of a CAT box, TATA box and  
XX transcription initiation site. The chimeric promoters are used in  
XX expression vectors for producing transgenic plants, such as  
XX dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,  
XX melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous  
XX species, e.g. wheat, barley, oat, rice, or corn.

XX Sequence 834 BP; 289 A; 175 C; 133 G; 237 T; 0 other;

Query Match 4.2%; Score 57; DB 21; Length 834;  
Best Local Similarity 100.0%; Pred. No. 3,1e-15;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 767 agataaccacttaagccacgactctgtgacatcatcatcctcaatcaca 824  
Rb 618 agataaccacttaagccacgactctgtgacatcatcctcaatcaca 674

RESULT 7

AAA6468

ID AAA6468 standard; DNA; 68 BP.

XX AAA6468;

XX 08-FEB-2001 (first entry)

XX Nucleotide sequence of the directional building block S3.

XX pete promoter; chimeric promoter; transgenic plant; MPl108;

XX plastocyanin gene promoter; PCR primer; ss.

XX Synthetic.

XX WO200056906-A1.

XX 28-SEP-2000.

XX 20-MAR-2000; 2000WO-1B00317.

XX 22-MAR-1999; 99FR-0003635.

XX (MERI-) MERISTEM THERAPEUTICS

XX Rance I, Gruber V, Theisen M;

XX WPI; 2000-587667/55.

XX Chimeric expression promoter for producing dicotyledonous and

XX monocotyledonous transgenic plants comprises a nucleic acid sequence

XX derived from a promoter of the pea plastocyanin gene

XX Claim 24; Page 73; 83pp; English.

XX The present sequence represents the directional building block S3,  
XX which is used to construct chimeric promoters of the invention in  
XX PCR reactions. The specification describes a chimeric expression  
XX promoter comprising a pete promoter of the pea plastocyanin gene, or  
XX comprising a G box operably or functionally linked upstream of a  
XX CAT box, TATA box and transcription initiation site. The chimeric  
XX promoters are used in expression vectors for producing transgenic  
XX plants, such as dicotyledonous species, e.g. potato, tobacco, cotton,  
XX lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower,  
XX and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.

XX Sequence 68 BP; 22 A; 19 C; 5 G; 22 T; 0 other;

Query Match 2.5%; Score 34; DB 21; Length 68;

Best Local Similarity 100.0%; Pred. No. 4,4e-05; Mismatches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 769 agatgagacatcatcatcctcaatcaca 823  
Rb 12 agatgagacatcatcatcctcaatcaca 45

RESULT 8

AAA6462

ID AAA6462 standard; DNA; 250 BP.

XX AAA6462;

XX 08-FEB-2001 (first entry)

XX Nucleotide sequence of the promoter MPl109.



DR WPI: 2000-587667/55.

PT Chimeric expression promoter for producing dicotyledonous and

PT monocotyledonous transgenic plants comprises a nucleic acid sequence

PT derived from a promoter of the pea plastocyanin gene -

PS Claim 2: Page 70; 83pp; English.

CC The present sequence represents the chimeric promoter Mpri1111. The

CC promoter is derived from the petE promoter from pea plastocyanin to 9x00,

CC by fusing the petE as-1 like and nos enhancer like elements to the

CC promoter Mpri1098 (comprising TATA and CAAT boxes of petE), and then

CC inserting a G box and fusing a fragment of 35S RNA of CMV. The petE

CC promoter directs cell-specific but not full light regulated expression in

CC transgenic tobacco plants. The promoter is used to construct chimeric

CC promoters of the invention. The specification describes a chimeric

CC expression promoter comprising a promoter of the pea plastocyanin gene,

CC or comprising a G box operably or functionally linked upstream of a CAAT

CC box, TATA box and transcription initiation site. The chimeric promoters

CC are used in expression vectors for producing transgenic plants, such as

CC dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,

CC melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous

CC species, e.g. wheat, barley, oat, rice, or corn.

SQ Sequence 280 BP; 88 A; 73 C; 42 G; 77 T; 0 other:

Query Match 2.3%; Score 31; DB 21; Length 280;

Best Local Similarity 100.0%; Pred No. 0 matches;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 790 cactctgtgcacatcattatctaatac 820  
|||||tggcgccgccccctttttttttttt

Db 68 cactctgtgcacatcattatctaatac 98

RESULT 11

AAA96465

ID AAA96465 standard; DNA: 296 BP

AC AAA96465;

XX 08-FEB-2001 (first entry)

DE Nucleotide sequence of the promoter Mpri1111.

KW PETE promoter; chimeric promoter; transgenic plant; Mpri1111;

KW plastocyanin gene promoter; ss.

XX Synthetic.

OS Pisum sativum.

PN Wo200056906-A1.

PD 28-SEP-2000.

Pf 20-MAR-2000; 2007WO 1P0621?

PR 22-MAR-1999; 99FR-0003635

PA (MERIT-) MERISTEM THERAPYUTICS.

PI Rance I, Gruber V, Theisen M;

DR WPI: 2000-587667/55.

PT Chimeric expression promoter for producing dicotyledonous and

PT monocotyledonous transgenic plants comprises a nucleic acid sequence

PT derived from a promoter of the pea plastocyanin gene -

PS Claim 2: Page 71; 83pp; English.

CC The present sequence represents the chimeric promoter Mpri1111. The

CC	promoters derived from the pete promoter from pea plastocyanin gene,
CC	by fusing the pete as 1 like and nos enhancer like elements to the
CC	primer Mpr106a (comprising TATA and CAAT boxes of petE), and then
CC	inserting a g box and fusing a fragment comprising a duplication of the
CC	element as2 and as1. The petE promoter directs cell-specific but not
CC	full light-regulated expression in transgenic tobacco plants. The
CC	petE promoter is used to construct chimeric promoters of the invention. The
CC	specification describes a chimeric expression promoter comprising a
CC	promoter of the pea plastocyanin gene, or comprising a g box operatively
CC	or functionally linked upstream of a CAAT box, TATA box and transcription
CC	initiation site. The chimeric promoters are used in expression vectors
CC	for producing transgenic plants, such as dicotyledonous species,
CC	e.g., potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,
CC	rape, beetroot, or sunflower; and monocotyledonous species, e.g., wheat,
CC	barley, oat, rice, or corn.
XX	
SQ	Sequence 296 BP: 94 A: 74 C: 45 G: 83 T: 0 other:
XX	
XX	Query Match: 2.3% Score 31: DN 21: Length 296:
XX	Best Local Similarity: 100.0%: E-Val: No.: 0.00084:
XX	Matches 31: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
Dy	790 cactctgtgcacatcattcataatc 820
Dd	
	84 cactctgtgcacatcattcataatc 114
XX	
RESULT 12	
ID	AAA96464 standard: DNA: 303 bp.
XX	AAA96464:
AC	AAA96464:
XX	
DT	08-FEB-2001 (first entry)
XX	
De	Nucleotide sequence of the promoter Mpr1153
XX	
KM	PETE Promoter: Chimeric promoter: transgenic plant: MPr1153:
KM	Plastocyanin gene promoter: ss.
XX	
OS	Synthetic:
OS	Psium sativum.
XX	
PN	W0200056906-A1.
XX	
PD	28-SEP-2000.
XX	
PF	29-MAR-2000: 2009WO-1B00317.
XX	
FX	22-MAR-1999: 99FR-0004635.
XX	
PA	(MERI-) MERISTEM THERAPYUS:
XX	
PI	Rance I, Gruber V, Weischen M:
XX	
XX	WFL: 2000 587667-755
XX	
FT	Chimeric expression promoter for producing heterozygous and
PT	monocytidicous transgenic plants comprises a nucleotide sequence
PT	derived from a promoter of the pea plastocyanin gene.
XX	
PS	Claim 2: Page 70: 83pp: English.
XX	
CC	The present sequence represents the chimeric promoter Mpr1153. The
CC	promoter is derived from the pete promoter from pea plastocyanin gene.
CC	The petE promoter directs cell-specific but not full light-regulated
CC	expression in transgenic tobacco plants. The promoter is used to
CC	construct chimeric promoters of the invention. The specification
CC	describes a chimeric expression promoter comprising a promoter of the
CC	pea plastocyanin gene, or comprising a g box operatively or functionally
CC	linked upstream of a CAAT box, TATA box and transcription initiation
CC	site. The chimeric promoters are used in expression vectors for producing



DE	Nucleotide sequence of the promoter Mp1143.			
XX				
KM	petE promoter; chimeric promoter; transgenic plant; Mp1143;			
KM	plastocyanin gene promoter; ss.			
XX				
OS	Synthetic.			
XX	Pisum sativum.			
PN	WO200056906-A1.			
XX				
PD	28-SEP-2000.			
XX				
PP	20-MAR-2000; 2000WO-1B0317.			
XX				
PR	22-MAR-1999; 99FR-0003635.			
XX				
PA	(MERI-) MERISTEM THERAPEUTICS.			
XX				
P1	Rance I, Gruber V, Theisen M;			
DR	WPI: 2000-587667/55.			
XX				
PT	Chimeric expression promoter for producing dicotyledonous and			
PT	monocotyledonous transgenic plants comprises a nucleic acid sequence			
PT	derived from a promoter of the pea plastocyanin gene			
XX				
PS	Claim 2; Page 72; 83pp; English.			
XX				
CC	The present sequence represents the chimeric promoter Mp1143. The			
CC	promoter is derived from the petE promoter from pea plastocyanin gene,			
CC	by fusing the petE as-1 like and nos enhancer like elements to the			
CC	promoter Mp1098 (comprising YATA and CAT boxes of petE), and then			
CC	inserting a G box and fusing a fragment comprising a duplication of the			
CC	element as2 and as1. A 72 bp fragment comprising the elements as-2, as-2			
CC	and as-1 was then deleted. The petE promoter directs cell-specific but			
CC	not full light-regulated expression in transgenic tobacco plants. The			
CC	promoter is used to construct chimeric promoters of the invention. The			
CC	specification describes a chimeric expression promoter comprising a			
CC	promoter of the pea plastocyanin gene, or comprising a G box operably			
CC	or functionally linked upstream of a CAT box, YATA box and transcription			
CC	initiation site. The chimeric promoters are used in expression vectors			
CC	for producing transgenic plants, such as dicotyledonous species,			
CC	e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,			
CC	rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,			
CC	barley, oat, rice, or corn.			
XX				
SO	Sequence 220 BP; 73 A; 60 C; 26 G; 61 T; 0 other;			

Query Match	1.9%;	Score 25;	DB 21;	Length 220;
Best Local Similarity	100.0%;	Freq. No. 0.37;		
Matches	25;	Conservative	0;	Mismatches
			0;	Indels
				0;
				Gaps
				0;

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OY      796 gtggacatctacattatctaattc 820
          |||
DB      14 gtggacatctacattatctaattc 38

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Search completed: September 1, 2002, 03:16:12  
Job time: 8261 sec

.

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on Jul 14, 2000 this sequence version replaced 41919290.  
(Contact: Harrison, M.)

FAX: 603.271.7210  
 Email: mjharrison@noble.com





QY 1250 ggaagaccattacattccagaacatgctgcttctccagaacatgcttctcagatga 1309  
 |||||||  
 Db 124 GGAACACACATTCATTCACAGAAAGTGGTTTCTCCACACCTTATCTTCGATCAA 183  
 |||||||

QY 1310 gacgaattccaagcgggtgatgc 1335  
 |||||||

Db 184 GAGGAGATTCAGAGGAGGCTTGATGC 209  
 |||||||

RESULT 13

BE633611 482 bp mRNA linear EST 19-DEC-2000  
 LOCUS NF058C04DT1034 Drought Medicago truncatula cDNA clone NF058C04DT  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BE633611  
 VERSION BE633611.1 GI:11897769  
 KEYWORDS EST.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;  
 Medicago.  
 1 (bases 1 to 482)  
 Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Heller, J.,  
 Flores, H.R., Jman, J.T., Weller, J.W. and May, G.D.  
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula drought library  
 Unpublished (2000)  
 CONTACT: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
 Insert Length: 482 Std Error: 0.00  
 Plate: 058 row: C column: 04  
 Seq primer: TCACACACCAACACCTATGAC  
 Location/Qualifiers  
 1..482  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone="NF058C04DT"  
 /tissue="leaf"  
 /tissue\_type="Plantlets"  
 /dev\_stage="Pooled timepoints"  
 /note="Vector: Lambda Zap; Contains a mixture of entire  
 plantlets harvested in a series of days post-watering  
 timepoints."

BASE COUNT 122 a 99 c 110 g 151 t

ORIGIN

Query Match 10.8% Score 146; Dh 10; Length 482;  
 Best local Similarity 100.0%; Pred. No. 1.9e-42;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 ttgcttgatgctagaaabagatgagcttcttctcagaacatgcttctcagatga 1249  
 |||||||  
 Db 149 TTGCTTGAGGCTTAGATGATGAGGATTTGATTTTAAATATTTAAATGAAATGAA 208  
 |||||||

QY 1250 ggaagaccattacattccagaacatgctgcttctccagaacatgcttctcagatga 1309  
 |||||||  
 Db 209 GGAACACACATTCATTCACAGAAAGTGGTTTCTCCACACCTTATCTTCGATCAA 258  
 |||||||

QY 1310 gacgaattccaagcgggtgatgc 1335  
 |||||||

Db 269 GAGGAGATTCAGAGGAGGCTTGATGC 294  
 |||||||

RESULT 14

BE316878 516 bp mRNA linear EST 21-DEC-2000  
 LOCUS NF067H081F1064 Developing leaf Medicago truncatula cDNA clone  
 DEFINITION NF067H081F5', mRNA sequence.  
 ACCESSION BE316878  
 VERSION BE316878.2 GI:11960234  
 KEYWORDS EST.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;  
 Medicago.  
 1 (bases 1 to 512)  
 Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Heller, G.D.,  
 Flores, H.R., Jman, J.T., Weller, J.W. and May, G.D.  
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula leaf library  
 Unpublished (2000)  
 On Jul 14, 2000 this sequence version replaced GI:9190655.  
 CONTACT: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
 Insert Length: 694 Std Error: 0.00  
 Plate: 067 row: B column: 08  
 Seq primer: TCACTAGGAAACATGATGAC  
 Location/Qualifiers  
 1..512  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone="NF067H081F"  
 /tissue="leaf"  
 /tissue\_type="Developing leaf"  
 /dev\_stage="Pooled developmental"  
 /note="Vector: Lambda Zap; Contains a mixture of very  
 young, developing, mature and senescing leaves."

BASE COUNT 137 a 119 c 111 g 145 t

ORIGIN

Query Match 10.8% Score 146; Dh 10; Length 512;  
 Best local Similarity 100.0%; Pred. No. 1.9e-42;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 ttgcttgatgctagaaabagatgagcttcttctcagaacatgcttctcagatga 1249  
 |||||||  
 Db 243 TTGCTTGAGGCTTAGATGATGAGGATTTGATTTTAAATATTTAAATGAAATGAA 302  
 |||||||

QY 1250 ggaagaccattacattccagaacatgctgcttctccagaacatgcttctcagatga 1309  
 |||||||  
 Db 303 GGAACACACATTCATTCACAGAAAGTGGTTTCTCCACACCTTATCTTCGATCAA 402  
 |||||||

QY 1310 gacgaattccaagcgggtgatgc 1335  
 |||||||

Db 363 GAGGAGATTCAGAGGAGGCTTGATGC 388  
 |||||||

RESULT 15

BE632144 516 bp mRNA linear EST 19-DEC-2000  
 LOCUS NF033F10C1F1080 Drought Medicago truncatula cDNA clone NF033F10C1  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BE632144  
 VERSION BE632144.1 GI:11896302  
 KEYWORDS EST.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophytes: *Matricaria* (Asteraceae); *Cere* (Cucurbitaceae); *Rhus* (Anacardiaceae); *Libanotis* (Fabaceae); *Papilionoidae*; *Trifolium* (Leguminosae).

REFERENCE	1 (bases 1 to 514)
AUTHORS	Tortorello, J. J. and

**TITLE**  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Flores, H.R., Loman, J., Welton, J.W., and May, G.D.

Medicamento: *Tramadol* (la deough) Library  
Unimelb (shod) (2000)

COMMINT  
Contact: May (11)  
Plant: Hialeah, Florida

The Samuel Roberts' No. 10 Foundation

2010 Sam Noble Pkwy  
Tel: 580 221 / 491

Fax: +80 221 7480  
 Email: [quincy@robilco.it](mailto:quincy@robilco.it)

Interest Income: \$140  
 Dividend Income: 100  
 Total Income: 240

Seq primer : 5'-TCTGAGGACATGGCATTCA-3'

PLANNING  
SCOTT  
LOCALIZATION/Quadrant 11615  
11.516

[illegible]

Case	Age	Sex	Duration of illness (years)	Onset	Course	Response to treatment	Outcome
1	12	F	1	Acute	Chronic	Partial	Recovery
2	15	M	2	Acute	Chronic	Partial	Recovery
3	18	F	3	Acute	Chronic	Partial	Recovery
4	20	M	4	Acute	Chronic	Partial	Recovery
5	22	F	5	Acute	Chronic	Partial	Recovery
6	25	M	6	Acute	Chronic	Partial	Recovery
7	28	F	7	Acute	Chronic	Partial	Recovery
8	30	M	8	Acute	Chronic	Partial	Recovery
9	32	F	9	Acute	Chronic	Partial	Recovery
10	35	M	10	Acute	Chronic	Partial	Recovery
11	38	F	11	Acute	Chronic	Partial	Recovery
12	40	M	12	Acute	Chronic	Partial	Recovery
13	42	F	13	Acute	Chronic	Partial	Recovery
14	45	M	14	Acute	Chronic	Partial	Recovery
15	48	F	15	Acute	Chronic	Partial	Recovery
16	50	M	16	Acute	Chronic	Partial	Recovery
17	52	F	17	Acute	Chronic	Partial	Recovery
18	55	M	18	Acute	Chronic	Partial	Recovery
19	58	F	19	Acute	Chronic	Partial	Recovery
20	60	M	20	Acute	Chronic	Partial	Recovery
21	62	F	21	Acute	Chronic	Partial	Recovery
22	65	M	22	Acute	Chronic	Partial	Recovery
23	68	F	23	Acute	Chronic	Partial	Recovery
24	70	M	24	Acute	Chronic	Partial	Recovery
25	72	F	25	Acute	Chronic	Partial	Recovery
26	75	M	26	Acute	Chronic	Partial	Recovery
27	78	F	27	Acute	Chronic	Partial	Recovery
28	80	M	28	Acute	Chronic	Partial	Recovery
29	82	F	29	Acute	Chronic	Partial	Recovery
30	85	M	30	Acute	Chronic	Partial	Recovery
31	88	F	31	Acute	Chronic	Partial	Recovery
32	90	M	32	Acute	Chronic	Partial	Recovery
33	92	F	33	Acute	Chronic	Partial	Recovery
34	95	M	34	Acute	Chronic	Partial	Recovery
35	98	F	35	Acute	Chronic	Partial	Recovery
36	100	M	36	Acute	Chronic	Partial	Recovery
37	102	F	37	Acute	Chronic	Partial	Recovery
38	105	M	38	Acute	Chronic	Partial	Recovery
39	108	F	39	Acute	Chronic	Partial	Recovery
40	110	M	40	Acute	Chronic	Partial	Recovery
41	112	F	41	Acute	Chronic	Partial	Recovery
42	115	M	42	Acute	Chronic	Partial	Recovery
43	118	F	43	Acute	Chronic	Partial	Recovery
44	120	M	44	Acute	Chronic	Partial	Recovery
45	122	F	45	Acute	Chronic	Partial	Recovery
46	125	M	46	Acute	Chronic	Partial	Recovery
47	128	F	47	Acute	Chronic	Partial	Recovery
48	130	M	48	Acute	Chronic	Partial	Recovery
49	132	F	49	Acute	Chronic	Partial	Recovery
50	135	M	50	Acute	Chronic	Partial	Recovery
51	138	F	51	Acute	Chronic	Partial	Recovery
52	140	M	52	Acute	Chronic	Partial	Recovery
53	142	F	53	Acute	Chronic	Partial	Recovery
54	145	M	54	Acute	Chronic	Partial	Recovery
55	148	F	55	Acute	Chronic	Partial	Recovery
56	150	M	56	Acute	Chronic	Partial	Recovery
57	152	F	57	Acute	Chronic	Partial	Recovery
58	155	M	58	Acute	Chronic	Partial	Recovery
59	158	F	59	Acute	Chronic	Partial	Recovery

1. The first part of the paper is devoted to the study of the properties of the function  $f(x)$  defined by the equation

✓Vociferantia: 1000000 ✓Carnivora: 1000000  
✓Fishes: 1000000 ✓Amphibia: 1000000  
✓Reptiles: 1000000 ✓Mammals: 1000000  
✓Birds: 1000000 ✓Insects: 1000000  
✓Plants: 1000000 ✓Fungi: 1000000  
✓Protists: 1000000 ✓Bacteria: 1000000  
✓Archaea: 1000000 ✓Eukarya: 1000000

$$\begin{aligned} & \left\{ \frac{\partial}{\partial t} + \nabla_{\vec{v}} \cdot \vec{v} - \Delta_{\vec{v}} \right\} f = 0 \\ & f|_{t=0} = f_0(\vec{x}, \vec{v}) \end{aligned}$$

DATE: 01/01/21	146	17	14
TIME: 15:11			

every match 10.00; score 10

West, David Samuel; Fred. N. Matthews 146; 'Conservative'; Mission

[illegible]

## 245. *Proteinuria in children*

**TABLE 1**

[illegible][illegible]

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 104

**The**  $\{A^{\alpha_1} A^{\alpha_2} \cdots A^{\alpha_n}\}$   $n$ -fold commutator,  $n \geq 0$ , is defined

Submitted: September 1, 2004

$$(\text{Fido} + \text{Jim}) : \{ (\text{Fido}, \text{Fido}), (\text{Fido}, \text{Jim}), (\text{Jim}, \text{Fido}), (\text{Jim}, \text{Jim}) \}$$

```

SeuratObj = completed = SeuratObject::
  CreateSeuratObject(counts = counts,
    meta.data = meta.data,
    verbose = FALSE)

```

De 3 AGAGAGAGAA



RESULT 5  
US-08-820-980-1  
Sequence 1, Application US/08820980  
Patent No. 5925388  
GENERAL INFORMATION:  
APPLICANT: Sylvain Moineau, Shirley A.  
APPLICANT: Walker, Ebenezer R. Vedamuthu,  
APPLICANT: and Peter A. Vandenberg  
TITLE OF INVENTION: Isolated DNA Encoding  
TITLE OF INVENTION: Enzyme For Phage  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian G. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB  
MEDIUM TYPE: storage  
COMPUTER: Acer  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/820,980  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/424,641  
FILING DATE: April 19, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian G. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: Quest 4.1-156  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5925388e  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2987 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
MOLECULE TYPE:  
US-08-820-980-1

Query Match 1.4% Score 19; DB 2; Length 2987;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 atgaattgataagaagtt 533  
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Db 1446 ATGAATTGATGAAGAAGTT 1464

RESULT 6  
US-08-826-439-1  
Sequence 1, Application US/08826439  
Patent No. 5972673  
GENERAL INFORMATION:  
APPLICANT: Sylvain Moineau, Shirley A.  
APPLICANT: Walker, Ebenezer R. Vedamuthu,  
APPLICANT: and Peter A. Vandenberg  
TITLE OF INVENTION: Isolated DNA Encoding  
TITLE OF INVENTION: Enzyme For Phage  
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ian G. McLeod  
STREET: 2190 Commons Parkway  
CITY: Okemos  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB  
MEDIUM TYPE: storage  
COMPUTER: Acer  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,439  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/424,641  
FILING DATE: April 19, 1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian G. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: Quest 4.1-156  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5972673e  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2987 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
MOLECULE TYPE:  
US-08-826-439-1

Query Match 1.4% Score 19; DB 2; Length 2987;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 atgaattgataagaagtt 533  
|||||  
Db 1446 ATGAATTGATGAAGAAGTT 1464

RESULT 7  
US-08-913-159-1  
Sequence 1, Application US/08913159  
Patent No. 6300109  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Plasmid-derived type II  
TITLE OF INVENTION: restriction modification systems from lactococcus lactis  
NUMBER OF SEQUENCES: 14  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn release #1.0, Version #1.30 (1990)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/913,159  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/9179/95  
FILING DATE: 17-FEB-1995  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3695 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

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1  PROPERTY: 110001
2  MOLECULE TYPE: DNA (genomic)
3  HYPOTHETICAL: NO
4  ANTI-SENSE: NO
5  ORIGINAL SOURCE:
6  ORGANISM: Lactococcus lactis subsp. cremoris
7  STRAIN: W9
8  FEATURE:
9  NAME/KEY: CDS
10 LOCATION: 1613..2419
11 IDENTIFICATION METHOD: expect:10001
12 OTHER INFORMATION: /product="L14A1" CAT# N 6 adenine methylase A"
13 OTHER INFORMATION: /protein="EXPERIMENTAL"
14 OTHER INFORMATION: /number="1"
15 OTHER INFORMATION: /standard name "Gene coding for M.L14A1A"
16 OTHER INFORMATION: /label="m.L14A1B"
17 FEATURE:
18 NAME/KEY: CDS
19 LOCATION: 1613..2419
20 IDENTIFICATION METHOD: expect:10001
21 OTHER INFORMATION: /product="L14A1" CAT# adenine methylase B"
22 OTHER INFORMATION: /protein="EXPERIMENTAL"
23 OTHER INFORMATION: /number="2"
24 OTHER INFORMATION: /standard name "Gene coding for M.L14A1B"
25 OTHER INFORMATION: /label="m.L14A1B"
26 FEATURE:
27 NAME/KEY: CDS
28 LOCATION: 2412..3425
29 IDENTIFICATION METHOD: expect:10001
30 OTHER INFORMATION: /product="L14A1" CAT# restriction endonuclease"
31 OTHER INFORMATION: /protein="EXPERIMENTAL"
32 OTHER INFORMATION: /number="3"
33 OTHER INFORMATION: /standard name "Gene coding for L14A1 restriction
34 OTHER INFORMATION: /label="L14A1"
35 US-08-913-159-1
36
37 Query Match 1-48: Score 19; 100.0% Length 4695%
38 Best Local Similarity 100.0% Prod. No. 17;
39 Matches 19; Conservation 0; Mismatches 0; Indels 0; Gaps 0;
40
41 515 atgaattgaggaaggaatt 533
42 11111111111111111111
43 ID 2118 ATGATGATGAAGACATT 2136
44
45 RESULT 8
46 US-08-913-159-4
47 Sequence 3; Application US/08014159
48 Patent No. 6400109
49 GENERAL INFORMATION:
50 APPLICANT:
51 TITLE OF INVENTION: Plasmid-derived type 11
52 NUMBER OF INVENTIONS: 14
53 NUMBER OF SEQUENCES: 14
54 COMPUTER READABLE FORM:
55 MEDIUM TYPE: Floppy disk
56 OPERATING SYSTEM: PC DOS/MS DOS
57 SOFTWARE: Patent In Release #1.0, Version #1.40 (EPO)
58 CURRENT APPLICATION DATA:
59 FILING DATE: 17 FEB 1995
60 APPLICATION NUMBER: 18-017,975
61 PRIORITY DATE: 17 FEB 1995

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1  INFORMATION FOR SEQ ID NO: 1:
2  SEQUENCE CHARACTERISTICS:
3  LENGTH: 4695 base pairs
4  TYPE: nucleic acid
5  STRANDEDNESS: double
6  PROPERTY: 110001
7  MOLECULE TYPE: DNA (genomic)
8  HYPOTHETICAL: NO
9  ANTI-SENSE: NO
10 ORIGINAL SOURCE:
11 ORGANISM: Lactococcus lactis subsp. cremoris
12 STRAIN: W9
13 FEATURE:
14 NAME/KEY: CDS
15 LOCATION: 1613..2419
16 IDENTIFICATION METHOD: expect:10001
17 OTHER INFORMATION: /product="L14A1" CAT# adenine methylase A"
18 OTHER INFORMATION: /protein="EXPERIMENTAL"
19 OTHER INFORMATION: /number="1"
20 OTHER INFORMATION: /standard name "Gene coding for M.L14A1A"
21 OTHER INFORMATION: /label="m.L14A1B"
22 US-08-913-159-4
23
24 Query Match 1-48: Score 19; 100.0% Length 4695%
25 Best Local Similarity 100.0% Prod. No. 17;
26 Matches 19; Conservation 0; Mismatches 0; Indels 0; Gaps 0;
27
28 515 atgaattgaggaaggaatt 533
29 11111111111111111111
30 ID 2118 ATGATGATGAAGACATT 2136
31
32 RESULT 9
33 US-08-913-159-5
34 Sequence 5; Application US/08913159
35 Patent No. 6400109
36 GENERAL INFORMATION:
37 APPLICANT:
38 TITLE OF INVENTION: Plasmid-derived type 11
39 NUMBER OF INVENTIONS: 14
40 NUMBER OF SEQUENCES: 14
41 COMPUTER READABLE FORM:
42 MEDIUM TYPE: Floppy disk
43 OPERATING SYSTEM: PC DOS/MS DOS
44 SOFTWARE: Patent In Release #1.0, Version #1.40 (EPO)
45 CURRENT APPLICATION DATA:
46 FILING DATE:
47 PRIOR APPLICATION DATA:
48 APPLICATION NUMBER: US/08/913,159
49 FILING DATE:
50 APPLICATION NUMBER: 18-017,975
51 FILING DATE: 17 FEB 1995
52 INFORMATION FOR SEQ ID NO: 5:
53 SEQUENCE CHARACTERISTICS:
54 LENGTH: 4695 base pairs
55 TYPE: nucleic acid
56 STRANDEDNESS: double
57 PROPERTY: 110001
58 MOLECULE TYPE: DNA (genomic)
59 HYPOTHETICAL: NO
60 ANTI-SENSE: NO
61 ORIGINAL SOURCE:
62 ORGANISM: Lactococcus lactis subsp. cremoris
63 STRAIN: W9
64 FEATURE:
65 NAME/KEY: CDS
66 LOCATION: 1649..2419
67 IDENTIFICATION METHOD: expect:10001
68 OTHER INFORMATION: /product="L14A1" CAT# adenine methylase B"
69 OTHER INFORMATION: /label="m.L14A1B"

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Source: Completed: September 1, 2002, 09:12:19  
Job time: 820 / sec

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/jorganism="synthetic construct"
/db_xref="taxon:32640"
/mole-"Sequence to be used as a promoter for regulational
expression"
BASE COUNT      390 a      141 c      145 g      295 t
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[illegible]

RESULT	3
AX105269	
LOC IS	731 bp
DEFINITION	Sequence 3 from Patent WO0125455.
ACCSSION	AX105269
VERSION	AX105269.1
KEYWORDS	GI:13921419
SOURCE	.
ORGANISM	synthetic construct synthetic construct artificial sequence. 1 (bases 1 to 731).
REFERENCE	Weizina,L.P. and J'Anouet,M A Promoter for regulating expression of foreign genes Patent: WO 0125455-A 3 12 APR 2001,
AUTHORS	Medicago Inc (CA)
TITLE	Location/Qualifiers
JOURNAL	1..731 /organism="synthetic construct" /db_xref="taxon:32630" /note="Sequence to be used as a promoter for regulating expression"
FEATURES	
source	
BASE COUNT	299 a 113 c 104 g 210 t
ORIGIN	

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	Best Local Similarity 100.0%	Prod No. 0			
	Matches 731	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	241	agagagaaaaagaaagacagagagataaaaaacataatgtagatagacacagaaactgttga	300		
Db	1	AGAGAGAAAAAGAGAAAGAGAGATATAAAACATAATGAGATATAGAGAAAGAACTGTGA	60		
QY	301	caaaagctgtaccacaaatagctgtcaaaatctcattgtgagacttgcacaaagctacaga	360		
Db	61	CAAAAGCTGTACCAAAATATTATTATAATATATTAGCAATTTGATMAAAATGATATTA	120		
QY	361	aataagqgttaattgcgttaaataaataagatgaagcattagagaaagctacacattaga	420		
Db	121	AATAGCGTTAATTGCGTGTAAATAAATAAGATGACGATGACGAGATGTACCAATTAGCA	180		
QY	421	gaactlltggcgaagctattaaaaagaaaaaataattatttlaaatagaagcttgaat	480		
Db	181	GAATTTTGGCAGAGCTATTAAAAAGAAACATAAATTTTTTAAANTTAAANTTAAAT	240		
QY	481	catttgatataacacatgtgatatttaataatgaattgaagaagagcttgatataagttgat	540		

[illegible]

RESULTS	4
AX036597	
LOCUS	AX036597 326 bp
DEFINITION	Sequence 3 from Patent FR2791358.
ACCESSION	AX036597
VERSION	AX036597 1 GI:1126192
KEYWORDS	
SOURCE	
ORGANISM	Synthetic construct.
REFERENCE	Synthetic construct.
AUTHORS	artificial sequence.
JOURNAL	1 (bases 1 to 326)
FEATURES	Rance,I., Tholsen,M. and Gruber,V. Patent: FR 2791358-A 3-29-SEP-2000; MERISTEM THERAPEUTICS (FR) Location/Qualifiers

Promoter	746-896	caaaacccccc	12630
	1..326	/note="The promoter Mpr1096 derived from the promoter pETB	
		by a deletion in 5' of the repeated invert sequences, of	
		the 'as-1 like' and ' enhancer like' elements borne by two	
		SpeI 403 bp fragments	
		promoter Mpr1096"	
HASH COUNT	111 d	91 c	38 g
ORIGIN			56 t
Query Match	5.9%; Score 57;	Dt 6;	Length 326;
Best local Similarity	100.0%;	Prod. No. 3.7e-16;	
Matches 57; Conservative	0;	Mismatches	0;
		Indels	0;
		Gaps	0;
Oy	759 agataaccactttaaacgagcgcctcgaggacatcatatcataatcacaca	815	
Dh	110 AGATTAACCCATTAAAGCTGCAATGTCTTGAACAATTTAATTATAATCAAC	166	

[illegible][illegible]

repeat_region	174	208	224	261	276	291	306	321	336	351	366	381	396	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	417	401	
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Db 91 CACTGTGTGACATCTACATTAATC 121

## RESULT 15

AX036609

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

MERISTEM

THERAPEUTICS (FR)

Location/Qualifiers

1..72

/organism="synthetic construct"

/db\_xref="taxon:32630"

/note="directional building block oligonucleotide for the construction of promoters by

1b-PCR"

BASIC COUNT

ORIGIN

22 a

20 c

10 g

20 t

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Gaps

Incls

Db

1

CTGTGTGACATCTACATTAATC

27

786

ctgtgtgacatctacatctaattc

812

1

ctgtgtgacatctacatctaattc

27

2.8%

Score 27

DB 6

Length 72

100.0%

Prod No 0.07

0

Mismatches

0

Incls

0

Gaps

0

Incls

0

Gaps

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Incls

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Gaps

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Gaps

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Gaps

0

Incls

0

Gaps

0

Search completed: September 1, 2002, 03:06:55  
Job time: 12052 sec

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XX 08-FEB-2001 (first entry)  
 DE Nucleotide sequence of the pete promoter from plastocyanin gene.  
 DE pete promoter, chimeric promoter, transgenic plant;  
 KM plastocyanin gene promoter; ss.  
 XX Plasm salivum.  
 XX WO200056906-A1.  
 XX 28-SEP-2000.  
 XX 20-MAR-2000; 2000WO-1B00317.  
 XX 22-MAR-1999; 99FR-0003635.  
 XX (MERI-) MERISTEM THERAPEUTICS.  
 XX Rance I, Gruber V, Theisen M;  
 PI WPI; 2000-587667/55.  
 XX Chimeric expression promoter for producing dicotyledonous and  
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence  
 PT derived from a promoter of the pea plastocyanin gene  
 PS Claim 1; Page 65; 83pp; English  
 XX The present sequence represents the pete promoter from the pea  
 CC plastocyanin gene. The promoter directs cell-specific but not full  
 CC light-regulated expression in transgenic tobacco plants. The promoter  
 CC is used to construct chimeric promoters of the invention. The  
 CC specification describes a chimeric expression promoter comprising a  
 CC promoter of the pea plastocyanin gene, or comprising a 6 box operably  
 CC or functionally linked upstream of a CAAT box, TATA box and  
 CC transcription initiation site. The chimeric promoters are used in  
 CC expression vectors for producing transgenic plants, such as  
 CC dicotyledonous species, e.g., potato, tobacco, cotton, lettuce, tomato,  
 CC melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous  
 CC species, e.g., wheat, barley, oat, rice, or corn.  
 XX Sequence 834 BP; 289 A; 175 C; 133 G; 237 T; 0 other;  
 SO

Query Match 5.9%; Score 57; FR 21; Length 834;  
 Best Local Similarity 100.0%; Pred. No. 166-14;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 agataaccacitlaagccacgactctgagacatctaatatctaatcaca 815  
 Db 618 agataaccacitlaagccacgactctgagacatctaatatctaatcaca 674

RESULT 7  
 AAAG6468  
 ID AAA96468 standard; DNA: 68 BP.  
 XX AAA96468;  
 XX 08-FEB-2001 (first entry)  
 DE Nucleotide sequence of the directional building block S3.  
 XX pete promoter; chimeric promoter; transgenic plant; MPT1108;  
 KM plastocyanin gene promoter; PCR primer; ss.  
 XX Synthetic.  
 XX WO200056906-A1.  
 XX 28-SEP-2000.

XX 20-MAR-2000; 2000WO-1B00317.  
 XX 22-MAR-1999; 99FR-0003635.  
 XX (MERI-) MERISTEM THERAPEUTICS.  
 XX Rance I, Gruber V, Theisen M;  
 PI WPI; 2000-587667/55.  
 XX Chimeric expression promoter for producing dicotyledonous and  
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence  
 PT derived from a promoter of the pea plastocyanin gene  
 PS Claim 24; Page 73; 83pp; English.  
 XX The present sequence represents the directional building block S3,  
 CC which is used to construct chimeric promoters of the invention in  
 CC PCR reactions. The specification describes a chimeric expression  
 CC promoter comprising a pete promoter of the pea plastocyanin gene, or  
 CC comprising a 6 box operably or functionally linked upstream of a  
 CC CAAT box, TATA box and transcription initiation site. The chimeric  
 CC promoters are used in expression vectors for producing transgenic  
 CC plants, such as dicotyledonous species, e.g., potato, tobacco, cotton,  
 CC lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower,  
 CC and monocotyledonous species, e.g., wheat, barley, oat, rice, or corn.  
 XX Sequence 68 BP; 22 A; 19 C; 5 G; 22 T; 0 other;  
 SO

Query Match 3.5%; Score 34; DR 21; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 94-05;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 762 cactctgtagacacatctaatatctaatcaca 815  
 Db 12 cactctgtagacacatctaatatctaatcaca 45

RESULT 8  
 AAA96462  
 ID AAA96462 standard; DNA: 250 BP.  
 XX AAA96462;  
 XX 08-FEB-2001 (first entry)  
 DE Nucleotide sequence of the promoter MPT1109.  
 XX pete promoter; chimeric promoter; transgenic plant; MPT1109;  
 KM plastocyanin gene promoter; ss.  
 XX Synthetic.  
 XX Plasm salivum.  
 XX WO200056906-A1.  
 XX 28-SEP-2000.  
 XX 20-MAR-2000; 2000WO-1B00317.  
 XX 22-MAR-1999; 99FR-0003635.  
 XX (MERI-) MERISTEM THERAPEUTICS.  
 XX Rance I, Gruber V, Theisen M;  
 PI WPI; 2000-587667/55.  
 XX Chimeric expression promoter for producing dicotyledonous and  
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence  
 PT derived from a promoter of the pea plastocyanin gene



SO Sequence 280 BP; 88 A; 74 C; 42 G; 77 T; 0 other;

Query Match 3.2%; Score 31; DB 21; Length 280;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 782 cactctgtgacacatctactataaacc 812

Db 68 cactctgtgacacatctactataaacc 98

RESULT 11

AAA96465

ID AAA96465 standard; DNA; 296 BP.

AC AAA96465;

DT 08-FEB-2001 (first entry)

DE Nucleotide sequence of the promoter MP1111.

KM petE promoter, chimeric promoter, transgenic plant; MP1111;

KW plastocyanin gene promoter; ss.

OS Synthetic.

OS Pisum sativum.

PN W0200056906-A1.

PD 28-SEP-2000.

PF 20-MAR-2000; 2000WO-1B00317

PR 22-MAR-1999; 99PR-0004635

PA (MER1-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Thelsen M;

DR WPI; 2000-587667/55.

PT Chimeric expression promoter for producing dicotyledonous and

PT monocotyledonous transgenic plants comprises a nucleic acid sequence

PT derived from a promoter of the pea plastocyanin gene

PS Claim 2; Page 71; 83pp; English.

CC The present sequence represents the chimeric promoter MP1111. The  
CC promoter is derived from the petE promoter from pea plastocyanin gene,  
CC by fusing the petE as-1 like and nos enhancer like elements to the  
CC promoter MP1098 (comprising TATA and CAAT boxes of petE), and then  
CC inserting a G box and fusing a fragment comprising a duplication of the  
CC element as2 and as1. The petE promoter directs cell-specific but not  
CC full light-regulated expression in transgenic tobacco plants. The  
CC promoter is used to construct chimeric promoters of the invention. The  
CC specification describes a chimeric expression promoter comprising a  
CC promoter of the pea plastocyanin gene, or comprising a G box operably  
CC or functionally linked upstream of a CAAT box, TATA box and transcription  
CC initiation site. The chimeric promoters are used in expression vectors  
CC for producing transgenic plants, such as dicotyledonous species,  
CC e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,  
CC rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,  
CC barley, oat, rice, or corn

SO Sequence 296 BP; 94 A; 74 C; 45 G; 83 T; 0 other;

Query Match 3.2%; Score 31; DB 21; Length 296;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 782 cactctgtgacacatctactataaacc 912

Db 84 cactctgtgacacatctactataaacc 114

RESULT 12

AAA96464

ID AAA96464 standard; DNA; 303 BP.

AC AAA96464;

DT 08-FEB-2001 (first entry)

DE Nucleotide sequence of the promoter MP11153

KM petE promoter, chimeric promoter, transgenic plant; MP11153;

KW plastocyanin gene promoter; ss.

OS Synthetic.

OS Pisum sativum.

PN W0200056906-A1.

PD 28-SEP-2000.

PF 20-MAR-2000; 2000WO-1B00317.

PR 22-MAR-1999; 99PR-0004635.

PA (MER1-) MERISTEM THERAPEUTICS

PI Rance I, Gruber V, Thelsen M;

DR WPI; 2000-587667/55.

PT Chimeric expression promoter for producing dicotyledonous and

PT monocotyledonous transgenic plants comprises a nucleic acid sequence

PT derived from a promoter of the pea plastocyanin gene

PS Claim 2; Page 70; 83pp; English.

CC The present sequence represents the chimeric promoter MP1153. The  
CC promoter is derived from the petE promoter from pea plastocyanin gene.  
CC The petE promoter directs cell-specific but not full light-regulated  
CC expression in transgenic tobacco plants. The promoter is used to  
CC construct chimeric promoters of the invention. The specification  
CC describes a chimeric expression promoter comprising a promoter of the  
CC pea plastocyanin gene, or comprising a G box operably or functionally  
CC linked upstream of a CAAT box, TATA box and transcription initiation  
CC site. The chimeric promoters are used in expression vectors for producing  
CC transgenic plants, such as dicotyledonous species, e.g. potato, tobacco,  
CC cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or  
CC sunflower, and monocotyledonous species, e.g. wheat, barley, oat, rice,  
CC or corn.

SO Sequence 303 BP; 101 A; 78 C; 41 G; 83 T; 0 other;

Query Match 3.2%; Score 31; DB 21; Length 303;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 782 cactctgtgacacatctactataaacc 812

Db 91 cactctgtgacacatctactataaacc 121

RESULT 13

AAA96470

ID AAA96470 standard; DNA; 72 BP.

AC AAA96470;

DT 08-FEB-2001 (first entry)



PT derived from a promoter of the pea plastocyanin gene  
 XX  
 PS Claim 2; Page 72; 83pp; English.  
 XX

CC The present sequence represents the chimeric promoter Mpr1143. The  
 CC promoter is derived from the petE promoter from pea plastocyanin gene,  
 CC by fusing the petE as-1 like and nos enhancer like elements to the  
 CC promoter Mpr1098 (comprising TATA and CAAT boxes of petE), and then  
 CC inserting a G box and fusing a fragment comprising a duplication of the  
 CC element as2 and as1. A 72 bp fragment comprising the elements as-2, as-2  
 CC and as-1 was then deleted. The petE promoter directs cell-specific but  
 CC not full light-regulated expression in transgenic tobacco plants. The  
 CC promoter is used to construct chimeric promoters of the invention. The  
 CC specification describes a chimeric expression promoter comprising a  
 CC promoter of the pea plastocyanin gene, or comprising a G box operably  
 CC or functionally linked upstream of a CAAT box, TATA box and transcription  
 CC initiation site. The chimeric promoters are used in expression vectors  
 CC for producing transgenic plants, such as dicotyledonous species,  
 CC e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,  
 CC rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,  
 CC barley, oat, rice, or corn.  
 XX

SQ Sequence 240 BP; 73 A; 30 C; 26 G; 61 T; 0 other;

# Query Match

Best Local Similarity 100.0%; Score 25; DB 21; Length 220;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 788 gtggacattacattatctaattc 812  
 ||||||||||||||||||||  
 DB 14 gtggacattacattatctaattc 38

Search completed: September 1, 2002, 03:16:22  
 Job time: 8271 sec

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text outlines various methods for organizing and storing data, including digital databases and physical filing systems.

2. The second section focuses on the role of technology in modern record management. It highlights how software solutions can streamline processes, reduce errors, and improve accessibility. Examples of specific tools and platforms are provided, along with a discussion on the security measures necessary to protect sensitive information.

3. The third part of the document addresses the challenges associated with long-term data retention. It explores the legal requirements for archiving records and the importance of regular audits to ensure compliance. The text also discusses the impact of technological advancements on the longevity of digital data and the need for robust backup strategies.

4. The final section provides a summary of key findings and offers recommendations for best practices. It stresses the importance of a proactive approach to record management, encouraging organizations to regularly review and update their policies and procedures. The document concludes by noting that effective record-keeping is not just a administrative task, but a critical component of organizational success.

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2002, 01:57:49 ; Search time 3236.08 seconds  
(without alignments)  
4062 374 Million cell updates/sec

Title: US-09-678-303-2

Perfect score: 971

Sequence: 1 CG3GCTGATATATATATG - AATCATATGAGAGAAATG 971

Scoring table: OLIGO\_NTC

Searched: 1776207 seqs, 674477642 residues

Word size: 0

Total number of hits satisfying chosen parameters: 27172414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

1: em\_estba:\*  
2: em\_estbun:\*  
3: em\_estlin:\*  
4: em\_estlun:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: qb\_est1:\*  
10: qb\_est12:\*  
11: qb\_hic:\*  
12: qb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrl:\*

Prod. No. is the number of results predicted by query. To have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	4.0	376	10	BE635678
2	35	3.6	611	10	BE635678
3	29	3.0	263	9	BE635678
4	29	3.0	341	10	BE635678
5	29	3.0	459	10	BE635678
6	29	3.0	478	10	BE635678
7	29	3.0	483	10	BE635678
8	29	3.0	603	9	BE635678
9	29	3.0	611	10	BE635678
10	29	3.0	637	10	BE635678
11	29	3.0	645	10	BE635678
12	29	3.0	683	10	BE635678
13	28	2.9	293	10	BE635678
14	28	2.9	359	9	BE635678
15	28	2.9	468	12	BE635678
16	28	2.9	667	10	BE635678
17	27	2.8	340	10	BE635678

18	27	2.8	514	10	BE635678
19	27	2.8	737	10	BE635678
20	27	2.8	774	10	BE635678
21	26	2.7	518	10	BE635678
22	25	2.6	159	10	BE635678
23	25	2.6	174	10	BE635678
24	25	2.6	334	9	BE635678
25	25	2.6	334	9	BE635678
26	25	2.6	346	9	BE635678
27	25	2.6	351	10	BE635678
28	25	2.6	351	10	BE635678
29	25	2.6	353	9	BE635678
30	25	2.6	356	10	BE635678
31	25	2.6	357	10	BE635678
32	25	2.6	358	10	BE635678
33	25	2.6	362	10	BE635678
34	25	2.6	368	10	BE635678
35	25	2.6	375	9	BE635678
36	25	2.6	385	10	BE635678
37	25	2.6	386	10	BE635678
38	25	2.6	392	10	BE635678
39	25	2.6	413	10	BE635678
40	25	2.6	417	10	BE635678
41	25	2.6	423	10	BE635678
42	25	2.6	433	10	BE635678
43	25	2.6	474	10	BE635678
44	25	2.6	512	10	BE635678
45	25	2.6	516	10	BE635678

#### ALIGNMENTS

RESULT 1  
LOCUS BE635678/c  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
barril medic.  
Medicago truncatula  
Bukariyola; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Rosidae; Eurosidae 1; Fabiales; Fabaceae; Papilionoideae; Trifoliales;  
Medicago.  
1 (bases 1 to 376)  
Torres-Jerez, J., Scott, A.D., Harris, A.W., Gonzalez, R.A., Bell, C.J.,  
Flores, H.R., Jimenez, J.L., Weller, J.W. and May, G.D.  
Expressed sequence tags from the Samuel Roberts Noble Foundation  
Medicago truncatula drought library  
Unpublished (2000)  
Contact: May GD  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2519 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 231 7391  
Fax: 580 231 7380  
Email: gdmay@noble.org  
Insert length: 376 Std Prot: 0.00  
Primer: TCAACAGAGAAACACTATGAC  
Seq primer: TCAACAGAGAAACACTATGAC  
Location/Qualifiers  
1..376  
/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/cdate="19990909"  
/clone="NP10940909"  
/cclone\_lib="Drought"  
/cclone\_lib="Plantlets"  
/cclone\_lib="Plantlets"  
/dev\_stage="Potted 16mepolys"  
/note="Yield 30g. Culture 4 weeks of culture  
plantlets harvested in a series of days post-planting"

#### FEATURES

source  
1..376  
/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/cdate="19990909"  
/cclone="NP10940909"  
/cclone\_lib="Drought"  
/cclone\_lib="Plantlets"  
/cclone\_lib="Plantlets"  
/dev\_stage="Potted 16mepolys"  
/note="Yield 30g. Culture 4 weeks of culture  
plantlets harvested in a series of days post-planting"



REFERENCE 1 (bases 1 to 341)  
 AUTHORS Torres-Jerez, I., Scott, A. D., Harris, A. R., Gonzalez, R. A., Bell, C. J., Flores, H. P., Imman, J. T., Weller, J. W. and May, G. D.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library  
 JOURNAL Unpublished (2000)  
 COMMENT On Jul 14, 2000 this sequence version replaced gi.3190043.  
 CONTACT: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
 Medicago genome initiative accession: MGI:518233  
 Insert Length: 609 Std Error: 0.00  
 Plate: 035 Row: F Column: 01  
 Seq primer: TCACACAGCAACGACCTATACAC.  
 Location/Qualifiers  
 1 341  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone="NF022H05FL"  
 /tissue="lib="Developing leaf"  
 /tissue\_type="leaf"  
 /dev\_stage="Pooled developmental"  
 /note="Vector: Lambda Zap, Contains a mixture of very young, developing, mature and senescing leaves"  
 BASE COUNT 90 a 81 c 73 g 97 t  
 ORIGIN

Query Match 3.0%, Score 29, DB 10, Length 341,  
 Best Local Similarity 100.0%, Pred. No. 5.5,  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 918 acacatcaagaagagaagactaataat 946  
 ||||||||||||||||||||||||||||  
 DB 16 ACACATCAACAAAGGAGACCTATATAT 44

RESULT 5  
 BI272586 369 bp mRNA linear EST 18 JUL 2001  
 LOCUS NF022H05FL1047 Developing flower Medicago truncatula cDNA clone  
 DEFINITION NF022H05FL 5', mRNA sequence.  
 ACCESSION BI272586  
 VERSION BI272586.1 GI:14882841  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
 Medicago.  
 1 (bases 1 to 369)  
 Torres-Jerez, I., Scott, A. D., Harris, A. R., Gonzalez, R. A., Bell, C. J., Flores, H. P., Imman, J. T., Weller, J. W. and May, G. D.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
 Insert Length: 369 Std Error: 0.00  
 Plate: 032 Row: H Column: 05  
 Seq primer: TCACACAGCAACGACCTATACAC.  
 Location/Qualifiers

FEATURES  
 source

source  
 1 369  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone="NF022H05FL"  
 /tissue="lib="Developing flower"  
 /tissue\_type="Developing flowers"  
 /dev\_stage="Developmentally pooled. Contains a mixture of very young, developing, fully-opened flowers and flowers in early transition into pods."  
 /note="Vector: Lambda Zap, cDNA was prepared from polyA-enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni Zap AR vector (Stratagene) and packaged using the GigaPack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the phage library using Xf vector using EXASSIST helper phage and the E. coli strain XL1-Hue MRF (Stratagene). Excised plasmids were plated using SOLR cells."

BASE COUNT 100 a 87 c 78 g 102 t 2 others  
 ORIGIN

Query Match 3.0%, Score 29, DB 10, Length 369,  
 Best Local Similarity 100.0%, Pred. No. 5.2,  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 918 acacatcaagaagagaagactaataat 946  
 ||||||||||||||||||||||||||||  
 DB 25 ACACATCAACAAAGGAGACCTATATAT 53

RESULT 6  
 BI270865 378 bp mRNA linear EST 18 JUL 2001  
 LOCUS NF002C02PL1020 Developing flower Medicago truncatula cDNA clone  
 DEFINITION NF002C02PL 5', mRNA sequence.  
 ACCESSION BI270865  
 VERSION BI270865.1 GI:14878866  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
 Medicago.  
 1 (bases 1 to 378)  
 Torres-Jerez, I., Scott, A. D., Harris, A. R., Gonzalez, R. A., Bell, C. J., Flores, H. P., Imman, J. T., Weller, J. W. and May, G. D.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
 Insert Length: 378 Std Error: 0.00  
 Plate: 002 Row: G Column: 02  
 Seq primer: TCACACAGCAACGACCTATACAC.  
 Location/Qualifiers  
 1 378  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone="NF002C02PL"  
 /tissue="lib="Developing flower"  
 /tissue\_type="Developing flowers"  
 /dev\_stage="Developmentally pooled. Contains a mixture of very young, developing, fully-opened flowers and flowers in early transition into pods."

FEATURES  
 source



REFERENCE 1 (bases 1 to 611)  
 AUTHORS Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library  
 JOURNAL Unpublished (2000)  
 COMMENT On Jul 13, 2000 this sequence version replaced gi:9119532.

CONTACT: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
 Medicago Genome Initiative accession: MGI:S:15-81  
 Insert Length: 657 Std Error: 0.00  
 Plate: 020 row: B column: 11  
 Seq primer: TCACTACAGAAACAGACTAATTAAT  
 location/Qualifiers  
 1..611  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone="NF020811F"  
 /clone\_lib="Developing leaf"  
 /tissue\_type="leaf"  
 /dev\_stage="Pooled developmental"  
 /note="Vector: lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

BASE COUNT 164 a 138 c 132 g 177 t

Query Match 3.0%; Score 29; DB 10; Length 611;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 918 acacatacaagaagaagactaat 946  
 ||||||||||||||||||  
 DB 34 ACACATACAAACAGACAGACTAATTAAT 62

RESULT 10  
 BG457563 637 bp mRNA linear EST 19-MAR-2001  
 LOCUS NF105G07PI.1P1054 phosphate starved leaf Medicago truncatula cDNA  
 DEFINITION clone NF105G07PI.5', mRNA sequence.  
 ACCESSION BG457563  
 VERSION BG457563.1 GI:13380804  
 KEYWORDS EST.  
 ORGANISM Medicago truncatula  
 barrel medic.  
 Medicago truncatula  
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,  
 Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,  
 Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifoliaceae,  
 Medicago.  
 1 (bases 1 to 637)  
 REFERENCE 1 (bases 1 to 637)  
 AUTHORS Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Harrison MU  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7325  
 Fax: 580 221 7380  
 Email: mjharrison@noble.org  
 Insert Length: 637 Std Error: 0.00  
 Plate: 105 row: G column: 07  
 Seq primer: TCACTACAGAAACAGACTAATTAAT

FEATURES  
 source  
 1..637  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone="NF105G07PI"  
 /clone\_lib="Phosphate starved leaf"  
 /tissue\_type="leaf"  
 /dev\_stage="Trifoliolate"  
 /note="Vector: lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoagland's solution containing only 200M potassium phosphate. RNA was prepared from above ground tissues."

BASE COUNT 178 a 148 c 128 g 182 t 1 others

Query Match 3.0%; Score 29; DB 10; Length 637;  
 Best Local Similarity 100.0%; Pred. No. 3.9;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 916 acacatacaagaagaagactaat 946  
 ||||||||||||||||||  
 DB 88 ACACATACAAACAGACAGACTAATTAAT 116

RESULT 11  
 BE249343 645 bp mRNA linear EST 13-JUL-2000  
 LOCUS NF014C09LE.1F1069 Developing leaf Medicago truncatula cDNA clone  
 DEFINITION NF014C09LE.5', mRNA sequence.  
 ACCESSION BE249343  
 VERSION BE249343.1 GI:9119403  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,  
 Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,  
 Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifoliaceae,  
 Medicago.  
 1 (bases 1 to 645)  
 REFERENCE 1 (bases 1 to 645)  
 AUTHORS Torres-Jerez, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
 Medicago Genome Initiative accession: MGI:S:14891  
 Insert Length: 645 Std Error: 0.00  
 Plate: 014 row: C column: 09  
 Seq primer: TCACTACAGAAACAGACTAATTAAT  
 location/Qualifiers  
 1..645  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone="NF014C09LE"  
 /clone\_lib="Developing leaf"  
 /tissue\_type="leaf"  
 /dev\_stage="Pooled developmental"  
 /note="Vector: lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

BASE COUNT 175 a 136 c 134 g 200 t

Query Match 3.0%; Score 29; DB 10; Length 645;



JOURNAL  
COMMENT

Medicago truncatula leaf library  
Unpublished (2000)  
On Apr. 14, 2003 this sequence version replaced gi.7558361  
Contact: May GN

Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7391  
Fax: 580 221 7380  
Email: gdmay@noble.org

FEATURES  
source

Insert Length: 713 Std Error: 0.00  
Plate: 016 row: 3 column: 16  
Seq primer: TCACACAGGAGAACGCTATGAC.  
Location/Qualifiers  
1..359

/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/clone\_lib="NF016610LF"  
/clone\_lib="Developing leaf"  
/issue\_type="leaf"  
/dev\_stage="Pooled developmental"  
/note="Vector: Lambda Zap; Contains a mixture of very  
young, developing, mature and senescing leaves."  
BASE COUNT 98 a 85 c 75 g 101 t  
ORIGIN

## Query Match

Best Local Similarity 100.0%; Score 28; DB 9; Length 359;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 919 cacatcaagaagagagactaatat 946  
|||||  
Db 1 CACATCAAGACAGACACTAATTAAT 28

REST LT 15  
A0841643 468 bp DNA linear GSS 27-SEP-1999  
LOCUS T137356b shotgun sub-library of BAC clone 72F02 Medicago truncatula  
DEFINITION genomic clone 72-F-02-084, DNA sequence.

ACCESSION A0841643  
VERSION A0841643.1 GI:5930668  
KEYWORDS GSS.  
SOURCE  
ORGANISM

Medicago truncatula  
barrel medic.  
Medicago truncatula  
Fukariyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,  
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,  
Rosidae, eurosids I, Fabales; Fabaceae; Papilionoideae; Trifoliales;  
Medicago.

REFERENCE 1 (bases 1 to 468)  
AUTHORS Kim, D., Choi, H., Peng, H., Ellis, L., and Cook, D.K.  
T TLE BAC survey sequencing of Medicago truncatula (1999c)  
JOURNAL Unpublished (1995)  
COMMENT Contact: Cook DR

The Crop Biotechnology Center  
Texas A&M University  
Department of Plant Pathology and Microbiology, Km 120 I., P.  
Peterson Bldg, College Station, TX 77843-2132, USA  
Tel: 409 845 8743  
Fax: 409 862 4790  
Email: dcook@ppserver.tamu.edu  
Other name: HSF-75-84, date: 7/2/99, Submitted to the Database of  
Genome Survey Sequences (GSS) on 09/27/99; More information is  
available at 'http://chrystle.tamu.edu/medicago'.  
Seq primer: pUC-C  
Class: BAC subclone.  
Location/Qualifiers

FEATURES  
source

1..468  
/organism="Medicago truncatula"  
/cultivar="genotype A17"  
/db\_xref="taxon:3880"  
/clone="72-F-02-084"

/clone\_lib="shotgun sub-library of BAC clone 72F02"  
/note="Vector: pUC18; BAC survey sequences were obtained  
from sheared BAC DNA subcloned into the SmaI site of  
pUC18. The template DNA for sequencing was obtained by PCR  
using universal primers. Sequencing reactions were primed  
from the pUC18 primer site (TGAAGAACATATGACATATATGCA)  
in the pUC18 polylinker."  
BASE COUNT 126 a 69 c 80 g 193 t  
ORIGIN

Query Match 2.9%; Score 28; DB 12; Length 468;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ataatgtatgtatgtatgtatgtatgt 299  
|||||  
Db 168 ATATATGTATGTATGTATGTATGTATGT 161

Search comp etcd: September 1, 2002, 01:57:53  
Job time: 10700 sec

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SeqCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 3, 2002 03:12:18 Search time 97.97 Seconds  
(without alignments)  
2487.850 Million cell updates/sec

Title: US-09-678-303-2  
Perfect score: 971

Sequence: 1 cggcctggtatattatg gattatctgagagaaatg g71

Scoring table: OLIGO, NUC  
Gapop 60.0, Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000300600

Post-processing: listing first 45 summaries

Database: Issued\_Patents\_NA \*

- 1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq \*
- 2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq \*
- 3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq \*
- 4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq \*
- 5: /cgn2\_6/ptodata/1/ina/PCUS.COMB.seq \*
- 6: /cgn2\_6/ptodata/1/ina/backfile1.seq \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	20	2.1	25	5 PCT-US91-03680-156	Sequence 156, App
2	19	2.0	1720	3 US-08-705-771-2	Sequence 2, Appl
3	19	2.0	2987	1 US-08-423-641B-1	Sequence 1, Appl
4	19	2.0	2987	2 US-08-820-980-1	Sequence 1, Appl
5	19	2.0	2387	2 US-08-826-439-1	Sequence 1, Appl
6	19	2.0	3695	4 US-08-913-159-1	Sequence 1, Appl
7	19	2.0	3695	4 US-08-913-159-3	Sequence 3, Appl
8	19	2.0	3695	4 US-08-913-159-5	Sequence 5, Appl
9	19	2.0	3695	4 US-08-913-159-7	Sequence 7, Appl
10	18	1.9	1064	1 US-08-378-588-15	Sequence 15, Appl
11	18	1.9	1064	2 US-08-811-054-15	Sequence 15, Appl
12	18	1.9	1064	5 PCT-US94-11121-15	Sequence 15, Appl
13	18	1.9	1270	1 US-08-378-588-23	Sequence 23, Appl
14	18	1.9	2270	5 US-08-811-094-23	Sequence 23, Appl
15	18	1.9	2270	5 PCT-US94-11121-23	Sequence 23, Appl
16	18	1.9	1884	1 US-07-704-288C-1	Sequence 1, Appl
17	18	1.9	1884	1 US-08-379-259-1	Sequence 1, Appl
18	18	1.9	3946	4 US-09-316-080-1	Sequence 1, Appl
19	18	1.9	8155	4 US-08-406-030A-23	Sequence 23, Appl
20	17	1.8	25	5 PCT-US91-03680-155	Sequence 155, App
21	17	1.8	25	5 PCT-US91-03680-157	Sequence 157, App
22	17	1.8	25	5 PCT-US91-03680-158	Sequence 158, App
23	17	1.8	352	4 US-08-396-452-2	Sequence 2, Appl
24	17	1.8	352	4 US-09-169-119-2	Sequence 2, Appl
25	17	1.8	564	4 US-08-617-86CB-12	Sequence 12, Appl
26	17	1.8	624	4 US-09-385-982-359	Sequence 359, App
27	17	1.8	723	4 US-09-328-111-338	Sequence 338, App

28	17	1.8	1425	2 US-08-883-515-1	Sequence 18, Appl
29	17	1.8	3835	3 US-08-723-624-18	Sequence 5, Appl
30	17	1.8	3630	4 US-08-474-000A-5	Sequence 5, Appl
31	17	1.8	3630	4 US-08-412-157-8	Sequence 19, Appl
32	17	1.8	3824	2 US-08-723-624-19	Sequence 13, Appl
33	17	1.8	5162	2 US-08-916-917-13	Sequence 13, Appl
34	17	1.8	5162	2 US-09-225-170-13	Sequence 5, Appl
35	17	1.8	4476	4 US-09-127-670-5	Sequence 20, Appl
36	17	1.8	6769	1 US-08-480-784-20	Sequence 20, Appl
37	17	1.8	6769	1 US-08-483-553-20	Sequence 20, Appl
38	17	1.8	6769	1 US-08-487-002-20	Sequence 20, Appl
39	17	1.8	6769	1 US-08-483-554B-20	Sequence 20, Appl
40	17	1.8	6769	1 US-08-488-011B-20	Sequence 20, Appl
41	17	1.8	6769	1 US-08-450-227-20	Sequence 20, Appl
42	17	1.8	6769	5 PCT-US95-10202-20	Sequence 20, Appl
43	17	1.8	6769	5 PCT-US95-10203-20	Sequence 20, Appl
44	17	1.8	6769	5 PCT-US95-10220-20	Sequence 20, Appl
45	17	1.8	17327	1 US-07-906-871-15	Sequence 15, Appl

#### ALIGNMENTS

RESULT 1  
PCT-US91-03680-156  
Sequence 156, Application PCT/US9103680  
GENERAL INFORMATION:  
APPLICANT: MATTEUCCI, MARK D.  
TITLE OF INVENTION: SEQUENCE-SPECIFIC NONHOMOLOGATED  
TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF  
TITLE OF INVENTION: DUPLEX DNA  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESS: MORRISON & FOERSTER  
STREET: 545 Middlefield Road, Suite 200  
CITY: Menlo Park  
STATE: California  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/03680  
FILING DATE: 19910924  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 4610-0011.40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-327-7250  
TELEFAX: 415-327-2951  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 156:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
PCT-US91-03680-156  
Query Match 2.1% Score 20; DB 5; Length 25;  
Best Local Similarity 100.0%; Pred No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
G 233 agagagagagagagagag 258  
|||||  
T 3 AGAGAGAGAGAGAGAGAG 22

## RESULT 2

US 08 705 771 2

Sequence 2, Application US 08/05/771

Patent No. 6054289

GENERAL INFORMATION:

APPLICANT: Paul Moore, Robert Gault, Bradford J.

APPLICANT: Dan N. and Tim Shain III

TITLE OF INVENTION: Human genes, Sequen-ces and

TITLE OF INVENTION: Expression products

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: CAROL A. JERNIG, PAUL, 1111 E. LAM,

ADDRESSEE: GEORGE STEWART &amp; CO. STEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIPS: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/705,771

FILING DATE: August 40 1996

CLASSIFICATION: 506

ATTORNEY/AGENT INFORMATION:

NAME: MILLINS, J.C.

REGISTRATION NUMBER: 4,0074

REFERENCE/BOOK REF NUMBER: 4,29800 (44) (FE196)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 974 994 170

TELEFAX: 974 994 1744

INFORMATION FOR SEQ ID NO: 25

SEQUENCE CHARACTERISTICS:

LENGTH: 1720 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US 08 705 771 2

## Query Match

Host Local Similarity: 100.0% Score 19; DB 4; Length 1720;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 442 TCAATGAAATTTTATTAAT 44

16 644 TCAATGAAATTTTATTAAT 66

## RESULT 3

US 08 424 641B 1

Sequence 1, Application US/08/424,641B

Patent No. 5824523

GENERAL INFORMATION:

APPLICANT: SYLVAIN MORGAN, Shirley A.

APPLICANT: Walter, Robert R. Veldman, Jr.

APPLICANT: and Peter A. Vandenburgh

TITLE OF INVENTION: Isolated DNA Encoding

TITLE OF INVENTION: Enzyme for Phage

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ian C. McLeod

STREET: 2190 Commons Parkway

CITY: Okemos

STATE: Michigan

COUNTRY: USA

ZIPS: 48864

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 400 Kb

MEDIUM TYPE: Storage

COMPUTER: Acer

OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/09/424,641B

FILING DATE: April 19, 1995

CLASSIFICATION: 445

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/066,480

FILING DATE: December 40, 1994

CLASSIFICATION: 445

ATTORNEY/AGENT INFORMATION:

NAME: Ian C. McLeod

REGISTRATION NUMBER: 20,941

REFERENCE/BOOK REF NUMBER: M 4,1 151

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 847-4100

TELEFAX: (517) 847-4104

INFORMATION FOR SEQ ID NO: 12

SEQUENCE CHARACTERISTICS:

LENGTH: 2987 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Double

TOPOLOGY: Linear

MOLECULE TYPE: Peptide

US 08 424 641B 1

## Query Match

Host Local Similarity: 100.0% Score 19; DB 1; Length 2987;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 507 ATGATGATGATGATGAT 525

DB 1446 ATGATGATGATGATGAT 1464

## RESULT 4

US 08 820 980 1

Sequence 1, Application US/08/820,980

Patent No. 5925888

GENERAL INFORMATION:

APPLICANT: SYLVAIN MORGAN, Shirley A.

APPLICANT: Walter, Robert R. Veldman, Jr.

APPLICANT: and Peter A. Vandenburgh

TITLE OF INVENTION: Isolated DNA Encoding

TITLE OF INVENTION: Enzyme for Phage

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ian C. McLeod

STREET: 2190 Commons Parkway

CITY: Okemos

STATE: Michigan

COUNTRY: USA

ZIPS: 48864

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 400 Kb

MEDIUM TYPE: Storage

COMPUTER: Acer

OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/09/820,980

FILING DATE:

CLASSIFICATION: 445

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/424,641

FILING DATE: April 19, 1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ian C. McLeod  
 REGISTRATION NUMBER: 20,931  
 REFERENCE/DOCKET NUMBER: Quest 4.1-156  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (517) 347-4100  
 TELEFAX: (517) 347-4103  
 TELETYPE: NO. 5925388C  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2987 base pairs  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Double  
 TOPOLOGY: Linear  
 MOLECULE TYPE:  
 US-08-820-980-1

Query Match: 2.0% Score 19, EB 2, Length 2987;  
 Best Local Similarity 10.0%; Prod. No. 21;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 atgaattgataaagaatt 525  
 |||||||  
 DB 1446 ATGAATTGATGAAGAGTT 1464

RESULT 5  
 US-08-826-439-1  
 Sequence 1, Application US/08826439  
 Patent No. 5972673  
 GENERAL INFORMATION:  
 APPLICANT: Sylvain Moineau, Shirley A.  
 APPLICANT: Walker, Ebenezer R. Vedamuthu,  
 APPLICANT: and Peter A. Vandenberg  
 TITLE OF INVENTION: Isolated DNA Encoding  
 TITLE OF INVENTION: Enzyme for Plaque  
 NUMBER OF INVENTIONS: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ian C. McLeod  
 STREET: 2190 Commons Parkway  
 CITY: Okemos  
 STATE: Michigan  
 COUNTRY: USA  
 ZIP: 48864  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
 MEDIUM TYPE: Storage  
 COMPUTER: Acer  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08,826,439  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/424,641  
 FILING DATE: April 19, 1995  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ian C. McLeod  
 REGISTRATION NUMBER: 20,931  
 REFERENCE/DOCKET NUMBER: Quest 4.1-156  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (517) 347-4100  
 TELEFAX: (517) 347-4103  
 TELETYPE: NO. 5972673C  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2987 base pairs

TYPE: Nucleic Acid  
 STRANDEDNESS: Double  
 TOPOLOGY: Linear  
 MOLECULE TYPE:  
 US-08-826-439-1

Query Match: 2.0% Score 19, EB 2, Length 2987;  
 Best Local Similarity 10.0%; Prod. No. 21;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 atgaattgataaagaatt 525  
 |||||||  
 DB 1446 ATGAATTGATGAAGAGTT 1464

RESULT 6  
 US-08-913-159-1  
 Sequence 1, Application US/08913159  
 Patent No. 6300109  
 GENERAL INFORMATION:  
 APPLICANT:  
 TITLE OF INVENTION: Plasmid-derived type II  
 TITLE OF INVENTION: restriction modification systems from *Lactococcus lactis*  
 NUMBER OF INVENTIONS: 14  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: MS-DOS/MS-PC  
 SOFTWARE: Patent in Release #1.0, Version #1.30 (EP)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/913,159  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PK 0179/95  
 FILING DATE: 17-FEB-1995  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3695 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *Lactococcus lactis* subsp. *cremoris*  
 STRAIN: W9  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 769..1620  
 IDENTIFICATION METHOD: experimental  
 OTHER INFORMATION: /codon\_start=769  
 OTHER INFORMATION: /product="L1A1-GATC-N-6-adenine methylase A"  
 OTHER INFORMATION: /evidence=EXPERIMENTAL  
 OTHER INFORMATION: /gene="ORF"  
 OTHER INFORMATION: /number=1  
 OTHER INFORMATION: /standard\_name="Gene coding for M.L1A1A"  
 OTHER INFORMATION: /label="m-l1a1A"  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1613..2419  
 IDENTIFICATION METHOD: experimental  
 OTHER INFORMATION: /codon\_start=1613  
 OTHER INFORMATION: /product="L1A1-GATC-adenine methylase B"  
 OTHER INFORMATION: /evidence=EXPERIMENTAL  
 OTHER INFORMATION: /gene="ORF"  
 OTHER INFORMATION: /number=2  
 OTHER INFORMATION: /standard\_name="Gene coding for M.L1A1B"  
 OTHER INFORMATION: /label="m-l1a1B"  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 2412..3323

IDENTIFICATION METHOD: expected  
 OTHER INFORMATION: /product "L1441 restriction endonuclease"  
 OTHER INFORMATION: /reference EXPERIMENTAL  
 OTHER INFORMATION: /name "p8p"  
 OTHER INFORMATION: /number 4  
 OTHER INFORMATION: /standard name "Gene coding for L1441 restriction  
 OTHER INFORMATION: endonuclease"  
 OTHER INFORMATION: /label L1441  
 US OR 913 159 1

Query Match 2.0% Score 192 DB 42 Length 46952  
 Best Local Similarity 100.0% Prod. No. 213  
 Matches 192 Conservation 0% Mismatches 0% Indels 0% Gaps 0%

US OR 913 159 1  
 DB 2118 ATGATGATGAAAGAAATCT 46

## RESULT 7

US OR 913 159 4  
 Sequence 8: Application us/or 913 159  
 Patent No. 6400109  
 GENERAL INFORMATION:  
 APPLICANT:  
 TITLE OF INVENTION: Plasmid derived type 11  
 TITLE OF INVENTION: restriction modification systems from Lactococcus lactis  
 NUMBER OF SEQUENCES: 14  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: Patent to be-patent #1.0, Version #1.40 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/6/913,159  
 FILING DATE:

## PRIORITY APPLICATION DATA:

APPLICATION NUMBER: EP 0 379 796  
 FILING DATE: 17 FEB 1994  
 INFORMATION FOR SEQ ID NO. 4  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4695 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGIN: SOURCE:  
 ORGANISM: Lactococcus lactis subsp. cremoris  
 STRAIN: W9  
 FEATURE:

NAME/KEY: COS  
 LOCATION: 1643..2419  
 IDENTIFICATION METHOD: expected  
 OTHER INFORMATION: /product "L1441" GATE adenine methylase B"  
 OTHER INFORMATION: /reference EXPERIMENTAL  
 OTHER INFORMATION: /number 2  
 OTHER INFORMATION: /standard name "Gene coding for M.L1441B"  
 OTHER INFORMATION: /label m.L1441B  
 US OR 913 159 4

## Query Match

Best Local Similarity 2.0% Score 192 DB 42 Length 46952  
 Matches 192 Conservation 0% Mismatches 0% Indels 0% Gaps 0%

US OR 913 159 4  
 DB 2118 ATGATGATGAAAGAAATCT 46

DB 2118 ATGATGATGAAAGAAATCT 2135

## RESULT 8

US OR 913 159 5  
 Sequence 9: Application us/or 913 159  
 Patent No. 6400109  
 GENERAL INFORMATION:  
 APPLICANT:  
 TITLE OF INVENTION: Plasmid derived type 11  
 TITLE OF INVENTION: restriction modification systems from Lactococcus lactis  
 NUMBER OF SEQUENCES: 14  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: Patent to be-patent #1.0, Version #1.40 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/6/913,159  
 FILING DATE:

## PRIORITY APPLICATION DATA:

APPLICATION NUMBER: EP 0 379 796  
 FILING DATE: 17 FEB 1994  
 INFORMATION FOR SEQ ID NO. 5  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4695 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGIN: SOURCE:  
 ORGANISM: Lactococcus lactis subsp. cremoris  
 STRAIN: W9  
 FEATURE:

NAME/KEY: COS  
 LOCATION: 1649..2419  
 IDENTIFICATION METHOD: expected  
 OTHER INFORMATION: /product "L1441" GATE adenine methylase B"  
 OTHER INFORMATION: /reference EXPERIMENTAL  
 OTHER INFORMATION: /number 2  
 OTHER INFORMATION: /standard name "Gene coding for M.L1441B"  
 OTHER INFORMATION: /label m.L1441B  
 US OR 913 159 5

## Query Match

Best Local Similarity 2.0% Score 192 DB 42 Length 46952  
 Matches 192 Conservation 0% Mismatches 0% Indels 0% Gaps 0%

US OR 913 159 5  
 DB 2118 ATGATGATGAAAGAAATCT 2135

US OR 913 159 7  
 Sequence 7: Application us/or 913 159  
 Patent No. 6400109  
 GENERAL INFORMATION:  
 APPLICANT:

TITLE OF INVENTION: Plasmid derived type 11  
 TITLE OF INVENTION: restriction modification systems from Lactococcus lactis  
 NUMBER OF SEQUENCES: 14  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: Patent to be-patent #1.0, Version #1.40 (EPO)  
 CURRENT APPLICATION DATA:



100 785 TAAATAAATAAATAAATAA A02

RESULT 12

US 09 478 508 24

Sequence 24, Application US/08478508

GENERAL INFORMATION:

APPLICANT: John, Mulyakal E.

TITLE OF INVENTION: TRANSGENIC COTTON PLANTS

TITLE OF INVENTION: PRODUCING HETEROLOGOUS PEROXIDASE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nicholas J. Seay, Quail Pass & Brady

STREET: First Wisconsin Plaza, One South

STREET: P.O. Box 2113

CITY: Madison

STATE: WI

COUNTRY: USA

ZIP: 53701 2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/11121

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27,486

REFERENCE/WORKET NUMBER: 1 229 9076 B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251 2484

TELEFAX: (608) 251 9166

INFORMATION FOR SEQ ID NO: 15

SEQUENCE CHARACTERISTICS:

LENGTH: 1064 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

PCT US94 11121 15

Query Match 1.00% Score 181 108 12 Length 1064

Best Local Similarity 100.00% Prod. No. 617

Matches 181 conservative 0 Mismatches 0 Gaps 0

US 939 TAAATAAATAAATAAATAA A06

100 785 TAAATAAATAAATAAATAA A02

RESULT 13

US 09 478 508 24

Sequence 24, Application US/08478508

GENERAL INFORMATION:

APPLICANT: John, Mulyakal E.

TITLE OF INVENTION: TRANSGENIC COTTON PLANTS

TITLE OF INVENTION: PRODUCING HETEROLOGOUS PEROXIDASE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nicholas J. Seay, Quail Pass & Brady

STREET: First Wisconsin Plaza, One South

STREET: P.O. Box 2113

CITY: Madison

STATE: WI

COUNTRY: USA

ZIP: 53701 2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/478,508

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27,486

REFERENCE/WORKET NUMBER: 1 229 9101 2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251 2484

TELEFAX: (608) 251 9166

INFORMATION FOR SEQ ID NO: 24

SEQUENCE CHARACTERISTICS:

LENGTH: 1270 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: tNA (transcript)

US 09 478 508 24

Query Match 1.00% Score 181 108 12 Length 1270

Best Local Similarity 100.00% Prod. No. 602

Matches 181 conservative 0 Mismatches 0 Gaps 0

US 939 TAAATAAATAAATAAATAA A06

100 791 TAAATAAATAAATAAATAA A08

RESULT 14

US 09 811 094 23

Sequence 23, Application US/08811094

Patent No. 5669720

GENERAL INFORMATION:

APPLICANT: John, Mulyakal E.

TITLE OF INVENTION: TRANSGENIC COTTON PLANTS

TITLE OF INVENTION: PRODUCING HETEROLOGOUS PEROXIDASE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nicholas J. Seay, Quail Pass & Brady

STREET: First Wisconsin Plaza, One South

STREET: P.O. Box 2113

CITY: Madison

STATE: WI

COUNTRY: USA

ZIP: 53701 2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/811,094

FILING DATE: 03 MAR 1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/478,509

FILING DATE: 25 JAN 1995

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27,486

REFERENCE/WORKET NUMBER: 1 229 9101 2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251 2484

TELEFAX: (608) 251 9166

Job time: 8223 sec

? INFORMATION FOR SEQ ID NO. 23:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 1270 base pairs  
 ? TYPE: nucleic acid  
 ? STRANDEDNESS: double  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: DNA (genomic)  
 ? US-08-811-094-23

Query Match 1.98; Score 18; DB 5; length 1270;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 939 taataataataatca 956  
 ||||||||||||||||  
 Db 991 TAAATAATAATAATCA 1008

RESULT 15  
 PCT-US94-11121-23  
 ? Sequence 23, Application PC/TUS9411121  
 ? GENERAL INFORMATION:  
 ? APPLICANT: John, Maliyakal E.  
 ? TITLE OF INVENTION: TRANSGENIC COTTON PLANTS  
 ? TITLE OF INVENTION: PEI-INDUCING HETEROLOGOUS PEROXIDASE  
 ? NUMBER OF SEQUENCES: 23  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Nicholas J. Scay, Charles & Hardy  
 ? STREET: First Wisconsin Plaza, One South  
 ? STREET: Pinckney St.,  
 ? STREET: P.O. Box 2113  
 ? CITY: Madison  
 ? STATE: WI  
 ? COUNTRY: USA  
 ? ZIP: 53701-2113  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: PCT/US94/11121  
 ? FILING DATE:  
 ? CLASSIFICATION:  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Scay, Nicholas J.  
 ? REGISTRATION NUMBER: 27,386  
 ? REFERENCE/DOCKET NUMBER: 11-229-9076-8  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (608) 251-2484  
 ? TELEFAX: (608) 251-9166  
 ? INFORMATION FOR SEQ ID NO: 23:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 1270 base pairs  
 ? TYPE: nucleic acid  
 ? STRANDEDNESS: double  
 ? TOPOLOGY: linear  
 ? MOLECULE TYPE: DNA (genomic)  
 ? PCT-US94-11121-23

Query Match 1.98; Score 18; DB 5; length 1270;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 939 taataataataatca 956  
 ||||||||||||||||  
 Db 991 TAAATAATAATAATCA 1008

Search completed: September 1, 2002, 03:12:34





[illegible][illegible]





repeat\_region 21..50  
/note="imperfect direct repeat 2"  
repeat\_region 25..62  
/note="imperfect direct repeat 3"  
old\_sequence 39..41  
/note="aca was aga in [1]"  
/calation-[1]  
59..88  
repeat\_region  
/note="imperfect direct repeat 2"  
94..139  
repeat\_region  
/note="imperfect direct repeat 1"  
114..142  
repeat\_region  
/note="imperfect direct repeat 2"  
130..159  
repeat\_region  
/note="imperfect direct repeat 2"  
134..171  
repeat\_region  
/note="imperfect direct repeat 3"  
723..730  
promoter  
/note="pol. TATA box"  
758..761  
misc\_feature  
/note="put. transcriptional start site"  
813..1319  
/note="precursor peptide (AA -69 to 99)"  
/codon\_start=1  
/protein\_id="CAA34212.1"  
/db\_xref="GI:20846"  
/db\_xref="SWISS-PROT:P16002"  
/translation="MAVSTSTVAIPSPGLTKTNATKVSAMAKIPTSTOSPLCVR  
ASLKDGVALVATASAVLASNAIAVEVLASDGLAFVPSLEVSAGETVVFNNNA  
GPHNVFDEDEIPAGVDASKISMPEEDLINRGFTYSKLDKGTITKTCYCSFHGAG  
MYGVTVN"

transit\_peptide 813..1019  
mat\_peptide 1020..1316  
/product="mature plastocyanin (AA 1-99)"  
BASE COUNT 460 a 299 c 283 g 463 t  
ORIGIN

Query Match 7.8%; Score 57; DB 8; Length 1505;  
Best Local Similarity 100.0%; Pred. No. 9; Bc-17;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 519 agataccacacttaagccacacactctgtgcacatcactatcctaaatcaca 575  
|||||  
Db 608 AGATAACCCACTTAAGCCACACCTGTGCACATCTACATTAATCACA 654

RESULT 9  
LOCUS AX036607 68 bp DNA linear PAT 15-NOV-2000  
DEFINITION Sequence 13 from Patent FR2791358.  
ACCESSION AX036607  
VERSION AX036607.1 GI:11226202  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct.  
artificial sequence.  
REFERENCE 1 (bases 1 to 68)  
Rance, I., Theisen, M. and Gruber, V.  
AUTHORS Patent: FR 2791358-A 13-SEP-2000;  
JOURNAL MERISTEM THERAPEUTICS (FR)  
FEATURES  
Location/Qualifiers  
1..68  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Directional building block S3-Directional building  
block oligonucleotide for the construction of promoters by  
1b-PCR"  
BASE COUNT 22 a 19 c 5 g 22 t  
ORIGIN

Query Match 4.7%; Score 34; DB 6; Length 68;

Best Local Similarity 100.0%; Pred No 1; Bc-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 542 cactctgtgcacatcactatcctaaatcaca 575  
|||||  
Db 12 CACTCTGTGCACATCTACATTAATCACA 45

RESULT 10  
LOCUS AX036607 250 bp DNA linear PAT 15-NOV-2000  
DEFINITION Sequence 6 from Patent FR2791358.  
ACCESSION AX036607  
VERSION AX036607.1 GI:11226195  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct.  
artificial sequence.  
REFERENCE 1 (bases 1 to 250)  
Rance, I., Theisen, M. and Gruber, V.  
AUTHORS Patent: FR 2791358-A 6-SEP-2000;  
JOURNAL MERISTEM THERAPEUTICS (FR)  
FEATURES  
Location/Qualifiers  
1..250  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
1..250  
/note="The promoter Mpr1109 differs from Mpr1108 by a  
deletion of 33 bp in the 5' UTR, 11 bp upstream of the  
point -41  
promoter Mpr1109"

BASE COUNT 81 a 67 c 31 g 71 t  
ORIGIN

Query Match 4.7%; Score 34; DB 6; Length 250;  
Best Local Similarity 100.0%; Pred No. 1; Bc-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 542 cactctgtgcacatcactatcctaaatcaca 575  
|||||  
Db 91 CACTCTGTGCACATCTACATTAATCACA 124

RESULT 11  
LOCUS AX036598 207 bp DNA linear PAT 15-NOV-2000  
DEFINITION Sequence 4 from Patent FR2791358.  
ACCESSION AX036598  
VERSION AX036598.1 GI:11226193  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct.  
artificial sequence.  
REFERENCE 1 (bases 1 to 207)  
Rance, I., Theisen, M. and Gruber, V.  
AUTHORS Patent: FR 2791358-A 4-SEP-2000;  
JOURNAL MERISTEM THERAPEUTICS (FR)  
FEATURES  
Location/Qualifiers  
1..207  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
1..207  
promoter  
/note="The promoter Mpr1098 of 207 bp only contains the  
'TATA' and 'CAAT' boxes and corresponds to a minimal  
reference promoter on the promoter pete.  
promoter Mpr1098"  
BASE COUNT 67 a 58 c 21 g 61 t  
ORIGIN

Query Match 4.4%; Score 32; DB 6; Length 207;  
Best Local Similarity 100.0%; Pred. No. 0; Bc-014;

[illegible]

RESULT	1,2				
AX036601		AX036601	280 bp	DNA	
DEFINITION		Sequence 7 from Patent FR279145B.			
ACCESSION		AX036601			
VERSION		AX036601.1	g1:11,261 bp		
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS		Rance, L., Thiesen, M., and Guber, V.			
JOURNAL		Patent : EP 2,791,408 A 2 29 SEP 2000;			
		MERKSTEM INFORMATIONICS (FR)			
FEATURES					
SOURCE					
		1..280			
		/organism "Synthetic construct"			
		db_xref "Genebank"			
		1..280			
		/note "The promoter Mpr1110 was created by inserting at position 99 bp of Mpr109g a element of 19 bp containing a GC box and by fusing a sequence of 44 bp of the RNA 35S promoter"			
		promoter Mpr1110"			
		BB 4 74 1 42 9 77 1			

Query Match	Similarity	100.0%	Prod. No.	0.0044	DB 6:	Length	280:
Matches	31:	Conservative	0:	Mismatches	0:	Indels	0:
QY	542	ccctctatgacacatcattatctaatc	572				
tbl	68	atctctctccacacatctattatctaatc	98				
RESULT 14							
AXO 66603							
LOCUS							
DEFINITION	AXO 66603		296 bp	DNA	linear	PAT 16-NOV 2003	
ACCESSION	Sequence 5	from Patent	FR2791758				
VERSION	AXO 66603		1				
KEYWORDS	AXO 66603.1		ct:11261-06				
SOURCE							
ORGANISM	Synthetic construct						
	Synthetic construct						
	artificial sequence						
REFERENCE	1 (bases 1 to 296)						
AUTHORS	Rance, L., Thomsen, M., and Gruber, V.						
JOURNAL	Patent: FR 2791758 A 1 29 SEP 2003						
	MERISTEM THERAPEUTICS (FR)						
	Location/Other effects						
FEATURES							
SOURCE	1..296						
	/organism="Synthetic construct"						
	296..296						
	296..296						
promoter	1..296						
	Location="Promoter" M91111 created by inserting at -99 bp						
	position of M91098; an 18 bp element containing a "G" box						
	and flusing a sequence of 58 bp (duplication of the element						
	552 and 553)						
	Promoter M91111"						
BASE COUNT	94 a	74 c	45 g		84 t		
ORIGIN							

[illegible]

	RESULT	14
AX046602	LOCUS	404 bp
	DEFINITION	Sequence from Patent FR2791858.
	ACCESSION	AX046602
	VERSION	AX046602.1 GI:1126197
	KEYWORDS	-
	SOURCE	synthetic construct
	ORGANISM	synthetic construct artificial sequence.
	REFERENCE	1 (bases 1 to 404) Rance, L., Theisen, M. and Gruber, V. Patent: FR 2791358 A B 29 SEP 2000; MERISTEM REGENERATION (FR)
FEATURES	location/orientations	
Source	1..404	CodonStart "synthetic construct"
	/db_xref="taxon:82640"	
	1..404	
Promoter	2905- <sup>"</sup>	The promoter MP1154 was obtained by fusing a sequence of 76 bp of the promoter polyA stretching from position 582 to position 510 bp modified by adjunction of a Tg box Promotor MP1154"
HASTE COUNT	101 a	76 c 41 g 84 t
ORIGIN		

Query Match	Similarity	100.0%	Frq. No.	0.00043	4.2%	Score 31	DB 6	Length 403	
Best Local	Similarity	100.0%	Frq. No.	0.00043	4.2%	Score 31	DB 6	Length 403	
Matches	31	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	542	CGCTCTGAGAGAGAGAGATATATAT	572	TTTTTTTTTTTTTTTTTTTTTTTTTTTT					
1b	91	CGCTCTGAGAGAGATATATATATAT	121						
RESULT 15									
AX036609									
LOCUS	AX036609	72 bp	DNA						
DEFINITION	Sequence 15 from Patent FR2791458.								
ACCESSION	AX036609								
VERSION	AX036609.1	GI:11246204							
KEYWORDS									
SOURCE									
ORGANISM	Synthetic construct.								
REFERENCE	Synthetic construct.								
AUTHORS	1 (bases 1 to 72).								
JOURNAL	Kaneko, T., Tsubota, M., and Gotoh, Y.								
	Patent: FR 2791458 A (5, 29 SEP. 2000).								
	MOBISTEM THERAPEUTICS (FR)								
FEATURES	Location/Qualifiers								
SOURCE	1..72								
	organism: "Synthetic construct"								
	/db_xref="taxon:42630"								
	/note="directional building block 85 directional building								
	block oligonucleotide for the construction of promoters by								
	1b-pcr"								
BASE COUNT	22 a	20 c	10 g	20 t					
ORIGIN									

Query Match:	4.78%	Score 41:	FB 6:	Length 296:
Query Match:	4.78%	Score 27:	DB 6:	Length 72:
Best Local Similarity	100.0%	Prod. No.	0.042:	
Matches 27:	Conservative	0:	Mismatches	0:
		0:	Indels	0:
		0:	Gaps	0:

Tue Sep 3 13:59:09 2002

us-09-678-303-3.oligo.rge

Page 7

OY 546 ctgtggcacatctacattatcraatc 572  
|||||  
Db 1 CTGTGGCACATCTACATTATCTAAATC 27

Search completed: September 1, 2002, 03:06:59  
Job time: 12056 sec







Oy	421	atlaattccctccccaaaaaaaacggtatattactaaaaaatcgaagccagttagg	480
Dd	661	attatacccctccaaaaaaacgggtatttactaaaaaatctaacgcagttagg	720
Oy	481	gataacatccaatccaacaacacacaaacctgatgagataaccatttaaggccac	540
Dd	721	galaaatccaatccaatccaatcacacaacctgatgagataaccatttaaggccac	780
Oy	541	gaactcgtagcaattatcatattctaataccacattcttcacacattctgagccaca	600
Dd	781	gaactcgtagcaattatcatattctaataccacattcttcacacattctgagccaca	840
Oy	601	caaaaaccaatccaatctttalacacccattctalaaaaaacacactttagagctacg	660
Dd	841	caaaaaccaatccaatctttatccaccattctataaaaaatcacactttagagctacg	900
Oy	661	acttgattcccttcaaacacacatacaagaagaagaaacatttaatttaalcattt	720
Dd	901	acttgattcccttcaaacacacatacaagaagaagaaacatttaatttaalcattt	960
Oy	721	gagagaaaatcg 731	
Dd	961	gagagaaaatcg 971	
RESULT 3			
AAS(2)126			
ID	AAS02126	standard; DNA: 1350 BP.	
XX			
AC	AAS02126:		
XX			
DT	18-JUN-2001	(first entry)	
XX			
DE	Promoter #1 for regulating expression of foreign genes		
XX			
KW	Promoter; transgenic plant; monocotyledon; dicotyledon; gymnosperm; ds		
OS	Synthetic.		
XX			
PN	WO200125455-A2.		
XX			
PD	12-Apr-2001.		
XX			
PF	02-OCT-2000; 2000WO-COJ1144.		
XX			
PR	04-OCT-1999; 99US-0157129.		
XX			
PA	(MEDIC-) MEDICAGO INV.		
XX			
P1	Vezina I., D'Aoust M;		
XX			
DR	WP1: 2001-266316/27.		
XX			
PT	Novel promoter for regulating expression of foreign genes in transgenic		
PT	organisms, more specifically in a leaf-specific manner in transgenic		
PT	plants -		
PS	Claim 1; Page 8; 9pp; English.		
XX			
CC	The sequence represents the coding sequence of promoter #1 for regulating		
CC	expression of foreign genes in transgenic organisms. The promoter is		
CC	useful for regulating the expression of foreign genes in transgenic		
CC	organisms, particularly plants, e.g. monocotyledons, dicotyledons or		
CC	gymnosperms, by preparing a transgenic organism using an expression		
CC	construct comprising the promoter and an open reading frame (ORF) of a		
CC	gene.		
XX			
Sequence	1350 BP; 482 A; 236 C; 230 G; 402 T; 0 other;		

Query Match	100.08;	Score 731;	DB 22;	Length 1350;
Best Local Similarity	100.08;	Pred. No. 4.9e-297;		

	Matches	731: Conservative	0: Mismatches	0: Indels	0: Gaps
QY	1	atgagagaaaaaagaagagagagatataaacaataatgtgtatgtatgagagagaattgtta	60		
Dh	249	atgagagaaaaaagaagagagatataaacaataatgtgtatgtatgagagagaattgtta	108		
QY	61	caaaagattgaccaaatalagtttgcacaatatacatatgaggaatttgcacaagaatgata	120		
Dh	309	caaaagattgaccaaatalagtttgcacaatatacatatgaggaatttgcacaagaatgata	168		
QY	121	aataagatttaatttactgttaaatgaatgaagatgaggaattatagaatgaatgaatga	180		
Dh	369	aataaagatttaatttactgttaaatgaatgaagatgaggaattatagaatgaatgaatga	428		
QY	181	gaatttttgcagatcatataaaaataaataaatttttttaatttaaaatttttttttttt	240		
Dh	429	gaatttttgcagatcatataaaaataaataaatttttttaatttaaaatttttttttttt	488		
QY	241	catltaagtaaaagatgattatattaatgaattgaataaagattgatttaaaattgaa	300		
Dh	489	catltaagtaaaagatgattatattaatgaattgaataaagattgatttaaaattgaa	548		
QY	301	tagtaattgaattttgtgtcaaatttaattgaatttgatcttttccctatatattgct	360		
Dh	549	tagtaattgaattttgtgtcaaatttaattgaatttgatcttttccctatatattgct	608		
QY	361	ccatagagatcaatttaactcattttatatattcatagatcaataaagaagaatacaagat	420		
Dh	609	ccatagagatcaatttaactcattttatatattcatagatcaataaagaagaatacaagat	668		
QY	421	atttaactctctaaadaaaaaaaatggtatattatataaataataagacctatgaag	480		
Dh	669	atttaactctctaaadaaaaaaaatggtatattatataaataataagacctatgaag	728		
QY	481	gataaacatcaatctcacccaatctcaaaaatctctgatatagataaacaccttaagacct	540		
Dh	729	gataaacatcaatctcacccaatctcaaaaatctctgatatagataaacaccttaagacct	788		
QY	541	gaactctgtgtgcacatcatatattataatcaacacattctctgtgcacattgaagctaa	600		
Dh	789	gaactctgtgtgcacatcatatattataatcaacacattctctgtgcacattgaagctaa	848		
QY	601	caaaaacccaatcacatctttatcaccatctttatataaaaaaacacactttgaaattat	660		
Dh	849	caaaaacccaatcacatctttatcaccatctttatataaaaaaacacactttgaaattat	908		
QY	661	acttgattctcttcaaacacacatacaaaagagagagatataatataatataatcatt	720		
Dh	909	acttgattctcttcaaacacacatacaaaagagagagatataatataatataatcatt	968		
QY	721	gagagagaatatg 731			
Dh	969	gagagagaatatg 979			
RESULT 4					
AAAG6459 standard: 10NA; 326 BP.					
AAAG6459:					
08-FEB-2001 (first entry)					
Nucleotide sequence of the promoter MP1096.					
PELE promoter; shrimp; promoter; transgenic plant; MP1096;					
plastocyanin gene promoter; ss.					
Synthetic.					
Pisum sativum.					
W0200056906.A1.					



CC light-regulated expression in transgenic tobacco plants. The promoter  
CC is used to construct chimeric promoters of the invention. The  
CC specification describes a chimeric expression promoter comprising a  
CC promoter of the pea plastocyanin gene, or comprising a G box operably  
CC or functionally linked upstream of a CAAT box, TATA box and  
CC transcription initiation site. The chimeric promoters are used in  
CC expression vectors for producing transgenic plants, such as  
CC dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,  
CC melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous  
CC species, e.g. wheat, barley, oat, rice, or corn.  
XX  
XX  
SQ Sequence 834 BP; 289 A; 175 C; 133 G; 237 T; 0 other;

Query Match 7.88; Score 57; DB 21; Length 834;  
Best Local Similarity 100.0%; Pred. No. 1.6e-14;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 519 agataaccacttaagccacgacatctatgacatcatatcataatcaca 575  
|||||  
Db 618 agataaccacttaagccacgacatctatgacatcatatcataatcaca 674

## RESULT 7

AAAh6468  
ID AAA96468 standard; DNA; 68 BP.

AC AAA96468;

DT 08-FEB-2001 (first entry)

DE Nucleotide sequence of the directional building block S3.

KW petE promoter; chimeric promoter; transgenic plant; MPr1108;

KM plastocyanin gene promoter; PCR primer; ss.

XX Synthetic.

PN W0200056906-A1.

PD 28-SEP-2000.

PE 20-MAR-2000; 2000W0-1B00317

PR 22-MAR-1999; 99PR-0003635.

PA (MER1-) MERISTEM THERAPEUTICS.

XX Rance I, Gruber V, Theisen M;

XX WPI; 2000-587667/55.

DR Chimeric expression promoter for producing dicotyledonous and

PT monocotyledonous transgenic plants comprises a nucleic acid sequence

XX derived from a promoter of the pea plastocyanin gene -

XX Claim 24; Page 73; 83pp; English.

CC The present sequence represents the directional building block S3,  
CC which is used to construct chimeric promoters of the invention in  
CC PCR reactions. The specification describes a chimeric expression  
CC promoter comprising a petE promoter of the pea plastocyanin gene, or  
CC comprising a G box operably or functionally linked upstream of a  
CC CAAT box, TATA box and transcription initiation site. The chimeric  
CC promoters are used in expression vectors for producing transgenic  
CC plants, such as dicotyledonous species, e.g. potato, tobacco, cotton,  
CC lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower,  
CC and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.  
XX  
XX  
SQ Sequence 68 BP; 22 A; 19 C; 5 G; 22 T; 0 other;

Query Match 4.78; Score 34; DB 21; Length 68;

Best Local Similarity 100.0%; Pred. No. 8.4e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 542 cactctgtgacatcatatcataatcaca 575  
|||||  
Db 12 cactctgtgacatcatatcataatcaca 45

## RESULT 8

AAAh6462  
ID AAA96462 standard; DNA; 250 BP.

AC AAA96462;

DT 08-FEB-2001 (first entry)

DE Nucleotide sequence of the promoter MPr1109.

KW petE promoter; chimeric promoter; transgenic plant; MPr1109;

KM plastocyanin gene promoter; ss.

XX Synthetic.

OS Pisum sativum.

PN W0200056906-A1.

PD 28-SEP-2000.

PE 20-MAR-2000; 2000W0-1B00317.

PR 22-MAR-1999; 99PR-0003635.

PA (MER1-) MERISTEM THERAPEUTICS.

XX Rance I, Gruber V, Theisen M;

XX WPI; 2000-587667/55.

DR Chimeric expression promoter for producing dicotyledonous and

PT monocotyledonous transgenic plants comprises a nucleic acid sequence

XX derived from a promoter of the pea plastocyanin gene -

XX Claim 2, Page 63; 83pp; English.

CC The present sequence represents the chimeric promoter MPr1109. The  
CC promoter is derived from the petE promoter from pea plastocyanin gene,  
CC by fusing the petE as-1 like and nos enhancer like elements to the  
CC promoter MPr1098 (comprising TATA and CAAT boxes of petE), and then  
CC deleting 33 bp from the 5'UTP. The petE promoter directs cell specific  
CC but not full light-regulated expression in transgenic tobacco plants.  
CC The promoter is used to construct chimeric promoters of the invention.  
CC The specification describes a chimeric expression promoter comprising  
CC a promoter of the pea plastocyanin gene, or comprising a G box operably  
CC or functionally linked upstream of a CAAT box, TATA box and  
CC transcription initiation site. The chimeric promoters are used in  
CC expression vectors for producing transgenic plants, such as  
CC dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,  
CC melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous  
CC species, e.g. wheat, barley, oat, rice, or corn.  
XX  
XX  
SQ Sequence 250 BP; 81 A; 67 C; 31 G; 71 T; 0 other;

Query Match 4.78; Score 34; DB 21; Length 250;  
Best Local Similarity 100.0%; Pred. No. 7.6e-05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 542 cactctgtgacatcatatcataatcaca 575  
|||||  
Db 91 cactctgtgacatcatatcataatcaca 124

RESULT 9



PF 20-MAR-2000; 2000WO-1B00317.  
 XX  
 PR 22-MAR-1999; 99PR-0003635.  
 XX  
 PA (MERI-) MERISTEM THERAPEUTICS  
 XX  
 PI Rance I, Gruber V, Theisen M;  
 XX  
 DR WPI: 2000-587667/55.  
 XX  
 PT Chimeric expression promoter for producing dicotyledonous and  
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence  
 PT derived from a promoter of the pea plastocyanin gene  
 XX  
 PS Claim 2; Page 71; 83pp, English.  
 XX  
 CC The present sequence represents the chimeric promoter Mpr111. The  
 CC promoter is derived from the pete promoter from pea plastocyanin gene,  
 CC by fusing the pete as-1 like and nos enhancer like elements to the  
 CC promoter Mpr1098 (comprising TATA and CAAT boxes of pete), and then  
 CC inserting a G box and fusing a fragment comprising a duplication of the  
 CC element as2 and as1. The pete promoter directs cell-specific but not  
 CC full light-regulated expression in transgenic tobacco plants. The  
 CC promoter is used to construct chimeric promoters of the invention. The  
 CC specification describes a chimeric expression promoter comprising a  
 CC promoter of the pea plastocyanin gene, or comprising a G box operably  
 CC or functionally linked upstream of a CAAT box, TATA box and transcription  
 CC initiation site. The chimeric promoters are used in expression vectors  
 CC for producing transgenic plants, such as dicotyledonous species,  
 CC e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,  
 CC rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,  
 CC barley, oat, rice, or corn.  
 XX  
 SQ Sequence 296 BP; 94 A; 74 C; 45 G; 83 T; 0 other;

Query Match 4.2%; Score 31; DB 21; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 0.0014;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 542 cactctgtggcacatcatatctaatac 572  
 ||||||||||||||||||||||||||||  
 DB 84 cactctgtggcacatcatatctaatac 114

RESULT 12  
 AAA96464  
 ID AAA96464 standard; DNA; 303 BP.  
 XX  
 AC AAA96464;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Nucleotide sequence of the promoter Mpr1153.  
 XX  
 KM pete promoter; chimeric promoter; transgenic plant; Mpr1153;  
 KM plastocyanin gene promoter; ss.  
 XX  
 OS Synthetic.  
 OS Pisum sativum.  
 XX  
 PN WO200056906-A1.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 20-MAR-2000; 2000WO-1B00317.  
 XX  
 PR 22-MAR-1999; 99PR-0003635.  
 XX  
 PA (MERI-) MERISTEM THERAPEUTICS.  
 XX  
 PI Rance I, Gruber V, Theisen M;  
 XX

DR WPI: 2000 587667/55.  
 XX  
 PT Chimeric expression promoter for producing dicotyledonous and  
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence  
 PT derived from a promoter of the pea plastocyanin gene  
 XX  
 PS Claim 2; Page 70; 83pp; English.  
 XX  
 CC The present sequence represents the chimeric promoter Mpr1153. The  
 CC promoter is derived from the pete promoter from pea plastocyanin gene.  
 CC The pete promoter directs cell-specific but not full light-regulated  
 CC expression in transgenic tobacco plants. The promoter is used to  
 CC construct chimeric promoters of the invention. The specification  
 CC describes a chimeric expression promoter comprising a promoter of the  
 CC pea plastocyanin gene, or comprising a G box operably or functionally  
 CC linked upstream of a CAAT box, TATA box and transcription initiation  
 CC site. The chimeric promoters are used in expression vectors for producing  
 CC transgenic plants, such as dicotyledonous species, e.g. potato, tobacco,  
 CC cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or  
 CC sunflower, and monocotyledonous species, e.g. wheat, barley, oat, rice,  
 CC or corn.  
 XX  
 SQ Sequence 303 BP; 101 A; 78 C; 41 G; 84 T; 0 other;

Query Match 4.2%; Score 31; DB 21; Length 303;  
 Best Local Similarity 100.0%; Pred. No. 0.0014;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 542 cactctgtggcacatcatatctaatac 572  
 ||||||||||||||||||||||||||||  
 DB 91 cactctgtggcacatcatatctaatac 121

RESULT 13  
 AAA96470  
 ID AAA96470 standard; DNA; 72 BP.  
 XX  
 AC AAA96470;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Nucleotide sequence of the directional building block S5.  
 XX  
 KM pete promoter; chimeric promoter; transgenic plant; Mpr1108;  
 KM plastocyanin gene promoter; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN WO200056906-A1.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 20-MAR-2000; 2000WO-1B00317.  
 XX  
 PR 22-MAR-1999; 99PR-0003635.  
 XX  
 PA (MERI-) MERISTEM THERAPEUTICS.  
 XX  
 PI Rance I, Gruber V, Theisen M;  
 XX  
 DR WPI: 2000-587667/55.  
 XX  
 PT Chimeric expression promoter for producing dicotyledonous and  
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence  
 PT derived from a promoter of the pea plastocyanin gene  
 XX  
 PS Claim 24, Page 75; 83pp, English.  
 XX  
 CC The present sequence represents the directional building block S5,  
 CC which is used to construct chimeric promoters of the invention in  
 CC PCR reactions. The specification describes a chimeric expression  
 CC promoter comprising a pete promoter of the pea plastocyanin gene, or



Search completed: September 1, 2002, 03:16:38  
Job time: 8287 sec

---







REFERENCE 1 (bases 1 to 341)  
 AUTHORS Torres-Jerez, I., Scott, A. B., Harris, A. R., Gonzales, R. A., Bell, C. J., Flores, H. P., Imman, J. T., Weller, J. W. and May, G. D.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library  
 JOURNAL unpublished (2000)  
 COMMENT On Jul 14, 2000 this sequence version replaced g10156043.  
 CONTACT: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
 Medicago Genome Initiative accession: MGI:S18233  
 Insert Length: 876, Std Error: 0.50  
 Plate: 015, row: F, column: 01  
 Seq primer: TCACGACCAAGACGACTAATGAC  
 Location/Qualifiers  
 1..341  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone\_lib="Developing leaf"  
 /issue\_type="leaf"  
 /dev\_stage="Pooled developmental"  
 /note="Vector: lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

BASE COUNT 90 a 81 c 73 g 97 t

ORIGIN

Query Match 4.0%; Score 29; DB 10; Length 341;  
 Best Local Similarity 100.0%; Pred. No. 5;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 678 acacatacaaaagagaactaataat 706  
 |||||||  
 Db 16 ACACATACAAAGACGACGACTAAT 44

RESULT 5  
 BI272586 369 bp mRNA linear EST 18 JUL 2001  
 LOCUS NF00236211F1047 Developing flower Medicago truncatula cDNA clone  
 DEFINITION NF00236211F1047, mRNA sequence.  
 ACCESSION BI272586  
 VERSION BI272586  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicot; Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.  
 1 (bases 1 to 359)  
 Flores, H. P., Imman, J. T., Weller, J. W. and May, G. D.  
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula flower library  
 JOURNAL unpublished (2000)  
 CONTACT: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
 Insert Length: 369, Std Error: 0.06  
 Plate: 022, row: H, column: 05  
 Seq primer: TCACGACCAAGACGACTAATGAC  
 Location/Qualifiers

FEATURES

source 1..369  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone\_lib="Developing flower"  
 /issue\_type="Developing flowers"  
 /dev\_stage="Developmentally pooled; Contains a mixture of very young, developing, fully opened flowers and flowers in early transition into pods."  
 /note="Vector: lambda Zap; cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Zap XR vector (Stratagene) and packaged using the QiaPack 111 Gold packaging extracts. Phagocids containing cDNA inserts were in vivo excised from the recombinant Zap XR vector using EXAssist helper phage and the E. coli strain XL1-blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

BASE COUNT 100 a 87 c 78 g 102 t 2 others

ORIGIN

Query Match 4.0%; Score 29; DB 10; Length 369;  
 Best Local Similarity 100.0%; Pred. No. 4.7;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 678 acacatacaaaagagaactaataat 706  
 |||||||  
 Db 25 ACACATACAAAGACGACGACTAAT 53

RESULT 6  
 BI270865 378 bp mRNA linear EST 18 JUL 2001  
 LOCUS NF00236211F1020 Developing flower Medicago truncatula cDNA clone  
 DEFINITION NF00236211F1020, mRNA sequence.  
 ACCESSION BI270865  
 VERSION BI270865  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicot; Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.  
 1 (bases 1 to 378)  
 Flores, H. P., Imman, J. T., Weller, J. W. and May, G. D.  
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula flower library  
 JOURNAL unpublished (2000)  
 CONTACT: May GD  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7391  
 Fax: 580 221 7380  
 Email: gdmay@noble.org  
 Insert Length: 378, Std Error: 0.00  
 Plate: 002, row: G, column: 02  
 Seq primer: TCACGACCAAGACGACTAATGAC  
 Location/Qualifiers  
 1..378  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone\_lib="Developing flower"  
 /issue\_type="Developing flowers"  
 /dev\_stage="Developmentally pooled; Contains a mixture of very young, developing, fully opened flowers and flowers in early transition into pods."

FEATURES

Note: "Vector": Lambda Zap2 cDNA was prepared from polyA<sup>+</sup> enriched, polyA<sup>+</sup> isolated samples of equivalent amounts of total RNA from very young, developing, fully opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Giga-pack 111 (Biolabs) packaging extracts. Phages containing cDNA inserts were in vitro excised from the recombinant Uni-Zap XR vector using EXASIST (Biolabs) phage and the E. coli strain XL1 Blue MR<sup>+</sup> (Stratagene). Excised plasmids were plated using "stock" cells.

Query Match: 4.0K; Score 29; 98.1%; Length 476;  
Best Local Similarity: 100.0%; Prod. No. 4; 7;  
Matches: 29; Conservative: 0; Mismatches: 0; Gaps: 0;

678 acatatacaaaagagagagagagat 706  
||||| ||||||| ||||||| ||||||| |||||||  
44 AACATACAAACACACACACATACATACAT 72

RESULT 7  
BE249400 483 bp mRNA linear EST 21 DEC 2000  
DEFINITION Medicago truncatula stem library  
NE014061E109 cDNA sequence  
BE249400  
VERSION BE249400.2 GI:11901928  
KEYWORDS EST  
SOURCE Medicago  
ORGANISM Medicago truncatula  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mammaliophyta; Eudicotyledons; Core eudicotyledons; Rosidae; Eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.

REFERENCE 1 (bases 1 to 483)  
Flores, H.R., J. Manzanillo, J.L. Weller, J.W. May, G.D., and J. A. Gonzalez, R.A., and May, G.D.,  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula stem library  
Unpublished (2000)  
Contact: May, G.D.  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7401  
Fax: 580 221 7480  
Email: gdmay@noble.org

Medicago Genome Initiative accession: MG153\_149/4  
Insert Length: 671; Std Error: 0.00  
Plate: 014; Row: 1; Column: 06  
Seq primer: TCATACAAACACATACATACAT

FEATURES  
SOURCE location/contig: flowers

1..483  
/organism "Medicago truncatula"  
/db\_xref "taxon:3880"  
/clone "NF014061E109"  
/clone\_lib "developing leaf"  
/tissue\_type "leaf"  
/dev\_stage "developing leaf"  
/note "Vector: Lambda Zap2; cDNA: a mixture of very young, developing, mature and senescing leaves."

BASE COUNT 144 a 112 c 99 g 144 t

Query Match: 4.0K; Score 29; 98.1%; Length 483;  
Best Local Similarity: 100.0%; Prod. No. 4;  
Matches: 29; Conservative: 0; Mismatches: 0; Gaps: 0;

678 acatatacaaaagagagagagat 706  
||||| ||||||| ||||||| ||||||| |||||||  
64 AACATACAAACACACACACATACATACAT 92

RESULT 8  
AW692904 603 bp mRNA linear EST 20 DEC 2000  
DEFINITION Medicago truncatula stem library  
NE060612S1 57 mRNA sequence  
AW692904  
VERSION AW692904.2 GI:11901928  
KEYWORDS EST  
SOURCE Medicago  
ORGANISM Medicago truncatula  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mammaliophyta; Eudicotyledons; Core eudicotyledons; Rosidae; Eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.

REFERENCE 1 (bases 1 to 603)  
Flores, H.R., J. Manzanillo, J.L. Weller, J.W. May, G.D., and J. A. Gonzalez, R.A., and May, G.D.,  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula stem library  
Unpublished (2000)  
Contact: May, G.D.  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7401  
Fax: 580 221 7480  
Email: gdmay@noble.org

Insert Length: 678; Std Error: 0.00  
Plate: 060; Row: 6; Column: 12  
Seq primer: TCATACAAACACATACATACAT

FEATURES  
SOURCE location/contig: flowers  
1..603  
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/db\_xref "taxon:3880"  
/clone "NF060612S1"  
/clone\_lib "developing stem"  
/tissue\_type "stem"  
/dev\_stage "developing leaf"  
/note "Vector: Lambda Zap2; cDNA: a mixture of internodal stem segments"

BASE COUNT 164 a 141 c 128 g 180 t

Query Match: 4.0K; Score 29; 98.1%; Length 603;  
Best Local Similarity: 100.0%; Prod. No. 4; 5;  
Matches: 29; Conservative: 0; Mismatches: 0; Gaps: 0;

678 acatatacaaaagagagagagat 706  
||||| ||||||| ||||||| ||||||| |||||||  
14 AACATACAAACACACACATACATACAT 41

RESULT 9  
BE249469 611 bp mRNA linear EST 21 DEC 2000  
DEFINITION Medicago truncatula stem library  
NE020811E1 57 mRNA sequence  
BE249469  
VERSION BE249469.2 GI:11901928  
KEYWORDS EST  
SOURCE Medicago  
ORGANISM Medicago truncatula  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mammaliophyta; Eudicotyledons; Core eudicotyledons;

Rosidae: eucosids I: Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

1 (bases 1 to 611)

REFERENCE  
AUTHORS  
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., and May, G.D.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation

TITLE  
Medicago truncatula leaf library

JOURNAL  
Unpublished (2000)

COMMENT  
On Jul 13, 2000 this sequence version replaced g1:919372.  
Contact: May GD  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7391  
Fax: 580 221 7380  
Email: gdmay@noble.org  
Medicago Genome Initiative accession: MG1:S15181  
Insert Length: 657 Std Error: 0.00  
Plate: 020 Row: B Column: 11  
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/clone="NF020B11LP"  
/clone\_lib="Developing leaf"  
/tissue\_type="leaf"  
/dev\_stage="Pooled developmental"  
/note="Vector, lambda Zap, contains a mixture of very young, developing, mature and senescing leaves"

BASE COUNT  
ORIGIN  
164 a 138 c 132 g 177 t

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Best Local Similarity 100.0%; Pred.No. 3.5; Mismatches 0; Indels 0; Gaps 0;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 678 acacatcaagaagaagactaatat 706  
|||||  
Db 34 ACACATCAAGACGACGCTATATAT 62

RESULT 10  
LOCUS  
BG457563 637 bp mRNA linear EST 19-MAR-2001

DEFINITION  
NF105G07P1P1054 Phosphate starved leaf Medicago truncatula cDNA

ACCESSION  
BG457563

VERSION  
BG457563.1 GI:13380804

KEYWORDS  
EST

SOURCE  
ORGANISM  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

REFERENCE  
AUTHORS  
Liu, J., Scott, A.B., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., May, G.D., and Harrison, M.T.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation

TITLE  
Medicago truncatula phosphate-starved leaf library

JOURNAL  
Unpublished (2000)

COMMENT  
Contact: Harrison MJ  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7325  
Fax: 580 221 7380  
Email: mtharrison@noble.org  
Insert Length: 637 Std Error: 0.00  
Plate: 105 Row: G Column: 07  
Seq primer: TCCACGCAAGACGCTATATAC

FEATURES  
Source  
1..637  
/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/clone="NF014C09LP"  
/clone\_lib="Phosphate starved leaf"  
/tissue\_type="leaf"  
/dev\_stage="Trifoliolate"  
/note="Vector, lambda Zap; At the trifoliolate stage, M truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1% Hoagland's solution containing only 200M potassium phosphate. RNA was prepared from above ground tissues."

BASE COUNT  
ORIGIN  
178 a 148 c 128 g 182 t

Query Match 4.0% Score 29; DB 10; Length 645;  
Best Local Similarity 100.0%; Pred.No. 3.4; Mismatches 0; Indels 0; Gaps 0;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 678 acacatcaagaagaagactaatat 706  
|||||  
Db 88 ACACATCAAGACGACGCTATATAT 116

RESULT 11  
LOCUS  
BE249343 645 bp mRNA linear EST 13-JUN-2000

DEFINITION  
NF014C09LP1069 Developing leaf Medicago truncatula cDNA clone

ACCESSION  
BE249343

VERSION  
BE249343.1 GI:9119403

KEYWORDS  
EST

SOURCE  
ORGANISM  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

REFERENCE  
AUTHORS  
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., and May, G.D.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation

TITLE  
Medicago truncatula leaf library

JOURNAL  
Unpublished (2000)

COMMENT  
Contact: May GD  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7391  
Fax: 580 221 7380  
Email: gdmay@noble.org  
Medicago genome Initiative accession: MG1:S14891  
Insert Length: 645 Std Error: 0.00  
Plate: 014 Row: C Column: 09  
Seq primer: TCACACGCAAGACGCTATATAC  
Location/Qualifiers  
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/db\_xref="taxon:3880"  
/clone="NF014C09LP"  
/clone\_lib="Developing leaf"  
/tissue\_type="leaf"  
/dev\_stage="Pooled developmental"  
/note="Vector, lambda Zap, contains a mixture of very young, developing, mature and senescing leaves"

BASE COUNT  
ORIGIN  
175 a 136 c 134 g 200 t

Query Match 4.0% Score 29; DB 10; Length 645;



JOURNAL Unpublished (2000)  
COMMENT On Apr 14, 2000 this sequence version replaced gi:7558361

BASE COUNT	ORIGIN
98 a	Young, developing, mature and senescing leaves.
85 c	
75 g	
101 t	

/clone\_11b" shotgun sub library of PAC clone 2729a."  
 /site "Vector.puc18". PAC safety screens were obtained  
 from sheared HAC DNA subcloned into the Sma site of  
 puc18. The template DNA for sequencing was obtained by PCR  
 using universal primers. Sequencing reactions were primed  
 from the puc18 primer site (GAGGAAAGGATATGATATATTAAG)  
 in the puc18 pol1 linker."

Query Match	1 A.	Score	29	TS	27	Length	448
Best Local Similarity	100.0%	Pred. No.	8				
Matches	28	Conservative	0				
		Mismatches	0				
		Indels	0				
		Gaps	0				

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GenCore version 4.5  
Copyright (c) 1994 - 2000 Compugen Ltd

QM nucleic - nucleic search, using SW model

Run #6 September 1, 2002, 03:12:34 : Search time 55.87 seconds  
(without alignments)  
1872 943 Million cell updates/sec

Title: US-09-678-303-3

Sequence: 1 agagagagaagaagagaggg ..... aatcatcttgagagaatg 731

Scoring table:

OLIGO\_NUC  
Gapop 60 0, Gapext 60 0

Searched: 383533 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Issued Patents\_NA:\*

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- 2: /cgn2\_6/prodata/1/ina/5B\_COMB seq:\*
- 3: /cgn2\_6/prodata/1/ina/5A\_COMB seq:\*
- 4: /cgn2\_6/prodata/1/ina/5B\_COMB seq:\*
- 5: /cgn2\_6/prodata/1/ina/5C\_COMB seq:\*
- 6: /cgn2\_6/prodata/1/ina/5D\_COMB seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	19	2.6	1720	3 US-08-705-771-2	Sequence 2, Appl
2	19	2.6	2987	1 US-08-424-641B-1	Sequence 1, Appl
3	19	2.6	2987	2 US-08-820-980-1	Sequence 1, Appl
4	19	2.6	2987	2 US-08-826-439-1	Sequence 1, Appl
5	19	2.6	3695	4 US-08-913-159-1	Sequence 1, Appl
6	19	2.6	3695	4 US-08-913-159-3	Sequence 3, Appl
7	19	2.6	3695	4 US-08-913-159-5	Sequence 5, Appl
8	19	2.6	3695	4 US-08-913-159-7	Sequence 7, Appl
9	19	2.5	25	5 PCT US91 03680-156	Sequence 156, App
10	18	2.5	1064	1 US-08-378-588-15	Sequence 15, Appl
11	18	2.5	1064	2 US-08-811-094-15	Sequence 15, Appl
12	18	2.5	1064	2 PCT US94 1112-15	Sequence 15, Appl
13	18	2.5	1270	1 US-08-378-588-23	Sequence 23, Appl
14	18	2.5	1270	1 US-08-811-094-23	Sequence 23, Appl
15	18	2.5	1270	5 PCT US94 11121-23	Sequence 23, Appl
16	18	2.5	1884	1 US-07-704-288C-1	Sequence 1, Appl
17	18	2.5	1884	1 US-08-479-759-1	Sequence 1, Appl
18	18	2.5	8355	4 US-08-406-030A-23	Sequence 23, Appl
19	17	2.3	25	5 PCT US91 03680-155	Sequence 155, App
20	17	2.3	25	5 PCT US91 03680-157	Sequence 157, App
21	17	2.3	25	5 PCT US91 03680-158	Sequence 158, App
22	17	2.3	352	1 US-08-396-452-2	Sequence 2, Appl
23	17	2.3	352	4 US-09-159-119-2	Sequence 2, Appl
24	17	2.3	564	3 US-08-617-866B-12	Sequence 12, Appl
25	17	2.3	624	4 US-09-385-982-359	Sequence 359, App
26	17	2.3	723	4 US-09-328-111-318	Sequence 338, App
27	17	2.3	1425	2 US-08-883-515-1	GENERAL INFORMAT

28	17	2.3	3025	2 US-08-723-624-14	Sequence 14, Appl
29	17	2.3	3630	4 US-08-424-900A-5	Sequence 5, Appl
30	17	2.3	4420	4 US-08-312-157-5	Sequence 5, Appl
31	17	2.3	3824	2 US-08-722-624-19	Sequence 19, Appl
32	17	2.3	5162	3 US-08-916-917-13	Sequence 13, Appl
33	17	2.3	5162	3 US-09-225-170-13	Sequence 13, Appl
34	17	2.3	6476	4 US-08-127-670-5	Sequence 5, Appl
35	17	2.3	5754	4 US-08-480-254-25	Sequence 25, Appl
36	17	2.3	6769	1 US-08-483-552-20	Sequence 20, Appl
37	17	2.3	6769	1 US-08-483-552-20	Sequence 20, Appl
38	17	2.3	6769	1 US-08-483-554B-20	Sequence 20, Appl
39	17	2.3	6769	1 US-08-484-011B-20	Sequence 20, Appl
40	17	2.3	6769	4 US-08-850-727-20	Sequence 20, Appl
41	17	2.3	6769	5 PCT US95-10302-20	Sequence 20, Appl
42	17	2.3	6769	5 PCT US95 10303-20	Sequence 20, Appl
43	17	2.3	6769	5 PCT US95 10320-20	Sequence 20, Appl
44	17	2.3	17327	1 US-07-906-871-15	Sequence 15, Appl
45	17	2.3	15231	3 US-09-128-155-16	Sequence 16, Appl

#### ALIGNMENTS

RESULT 1  
US-08-705-771-2  
Sequence 2, Application US/08705771  
Patent No. 6054289

GENERAL INFORMATION:  
APPLICANT: Paul Moore, Palmer Gentz, Hongjin Ji,  
APPLICANT: Jian Ni and Jing-Shan Hu  
TITLE OF INVENTION: Human Genes, Sequences and  
TITLE OF INVENTION: Expression Products  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CABELLA, BYRNE, BAIN, GILLILLAN,  
ADDRESSEE: CROCHIL, STEWART & OLSTERN  
STREET: 6 HICKORY FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/705,771  
FILING DATE: August 30, 1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-346 (PFI96)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 973-994-1700  
TELEFAX: 973-994-1744  
INFORMATION FOR SEQ ID NO. 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1720 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-705-771-2

Query Match: 2.6%; Score 19; DB 3; Length 1720;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 19; Conservative 2; Mismatch 0;  
CQ 92 tcatgaagaattacaa 110  
|||||

10 644 ATGATGAAATGAAACAC11 1463

# RESULT 2

11 US 08 424 641B 1

12 Sequence 1, Application US/00424641B

13 Patent No. 5925488

14 GENERAL INFORMATION:

15 APPLICANT: Sylvain Molinoux, Shireley A.

16 APPLICANT: Walker, Elizabeth R. Wadmuthe,

17 APPLICANT: and Peter A. Van denburgh

18 TITLE OF INVENTION: Isolated DNA encoding

19 TITLE OF INVENTION: Enzyme for Phago

20 NUMBER OF SEQUENCES: 12

21 CORRESPONDENCE ADDRESS:

22 ADDRESSEE: Ian C. McLeod

23 STREET: 2190 Commons Parkway

24 CITY: Okemos

25 STATE: Michigan

26 COUNTRY: USA

27 ZIP: 48864

28 COMPUTER RELEVABLE FORM:

29 MEDIUM TYPE: Diskette, 5.25 inch, 600 KB

30 MEDIUM TYPE: Storage

31 OPERATING SYSTEM: MS DOS

32 SOFTWARE: WordPerfect 5.1

33 CURRENT APPLICATION DATA:

34 APPLICATION NUMBER: US/08 424 641B

35 FILING DATE: April 19, 1995

36 CLASSIFICATION: 435

37 PRIORITY APPLICATION DATA:

38 APPLICATION NUMBER: 08/06 4400

39 FILING DATE: December 09, 1994

40 CLASSIFICATION: 435

41 ATTORNEY/AGENT INFORMATION:

42 NAME: Ian C. McLeod

43 REGISTRATION NUMBER: 20,941

44 REFERENCE/PACKET NUMBER: MT 4.1 151

45 TELECOMMUNICATION INFORMATION:

46 TELEPHONE: (517) 347 4100

47 TELEFAX: (517) 347 4100

48 TELEX: NO. 5925488

49 INFORMATION FOR SEQ ID NO. 1:

50 SEQUENCE CHARACTERISTICS:

51 LENGTH: 2987 base pairs

52 TYPE: Nucleic Acid

53 STRANDEDNESS: Double

54 TOPOLOGY: Linear

55 MOLECULE TYPE: TopoLibo

56 US 08 424 641B 1

57 Query Match: 2.5% Score 19; PH 1; Length 2987;

58 Best Local Similarity: 10.0%; Prod. No. 16;

59 Matches: 19; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

60 267 atgaattgaataaaat 285

61 111111111111111111

62 1446 ATGATGAAATGAAACAC11 1463

# RESULT 4

63 US 08 826 980 1

64 Sequence 1, Application US/00826980

65 Patent No. 5925488

66 GENERAL INFORMATION:

67 APPLICANT: Sylvain Molinoux, Shireley A.

68 APPLICANT: Walker, Elizabeth R. Wadmuthe,

69 APPLICANT: and Peter A. Van denburgh

70 TITLE OF INVENTION: Isolated DNA encoding

71 TITLE OF INVENTION: Enzyme for Phago

72 NUMBER OF SEQUENCES: 12

73 CORRESPONDENCE ADDRESS:

74 ADDRESSEE: Ian C. McLeod

75 STREET: 2190 Commons Parkway

76 CITY: Okemos

77 STATE: Michigan

78 COUNTRY: USA

79 ZIP: 48864

80 COMPUTER RELEVABLE FORM:

81 MEDIUM TYPE: Diskette, 5.25 inch, 600 KB

82 MEDIUM TYPE: Storage

83 OPERATING SYSTEM: MS DOS

84 SOFTWARE: WordPerfect 5.1

85 CURRENT APPLICATION DATA:

86 APPLICATION NUMBER: US/08 826 980

87 FILING DATE: April 19, 1995

88 CLASSIFICATION: 435

89 PRIORITY APPLICATION DATA:

90 APPLICATION NUMBER: 08/06 4400

91 FILING DATE: December 09, 1994

92 CLASSIFICATION: 435

93 ATTORNEY/AGENT INFORMATION:

94 NAME: Ian C. McLeod

95 REGISTRATION NUMBER: 20,941

96 REFERENCE/PACKET NUMBER: US/08 424 641

97 TELECOMMUNICATION INFORMATION:

98 TELEPHONE: (517) 347 4100

99 TELEFAX: (517) 347 4100

100 TELEX: NO. 5925488

101 INFORMATION FOR SEQ ID NO. 1:

102 SEQUENCE CHARACTERISTICS:

103 LENGTH: 2987 base pairs

104 TYPE: Nucleic Acid

105 STRANDEDNESS: Double

106 TOPOLOGY: Linear

107 MOLECULE TYPE: TopoLibo

108 US 08 826 980 1

109 Query Match: 2.5% Score 19; PH 1; Length 2987;

110 Best Local Similarity: 10.0%; Prod. No. 16;

111 Matches: 19; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

112 267 atgaattgaataaaat 285

113 111111111111111111

114 1446 ATGATGAAATGAAACAC11 1463

# RESULT 4

115 US 08 826 980 1

116 Sequence 1, Application US/00826980

117 Patent No. 5925488

118 GENERAL INFORMATION:

119 APPLICANT: Sylvain Molinoux, Shireley A.

120 APPLICANT: Walker, Elizabeth R. Wadmuthe,

121 APPLICANT: and Peter A. Van denburgh

122 TITLE OF INVENTION: Isolated DNA encoding

123 TITLE OF INVENTION: Enzyme for Phago

124 NUMBER OF SEQUENCES: 12

125 CORRESPONDENCE ADDRESS:

126 ADDRESSEE: Ian C. McLeod

127 STREET: 2190 Commons Parkway

128 CITY: Okemos

129 STATE: Michigan

130 COUNTRY: USA

131 ZIP: 48864

132 COMPUTER RELEVABLE FORM:

133 MEDIUM TYPE: Diskette, 5.25 inch, 600 KB

134 MEDIUM TYPE: Storage

135 OPERATING SYSTEM: MS DOS

136 SOFTWARE: WordPerfect 5.1

137 CURRENT APPLICATION DATA:

138 APPLICATION NUMBER: US/08 826 980

139 FILING DATE: April 19, 1995

140 CLASSIFICATION: 435

141 ATTORNEY/AGENT INFORMATION:

142 NAME: Ian C. McLeod

143 REGISTRATION NUMBER: 20,941

144 REFERENCE/PACKET NUMBER: US/08 424 641

145 TELECOMMUNICATION INFORMATION:

146 TELEPHONE: (517) 347 4100

147 TELEFAX: (517) 347 4100

148 TELEX: NO. 5925488

149 INFORMATION FOR SEQ ID NO. 1:

150 SEQUENCE CHARACTERISTICS:

151 LENGTH: 2987 base pairs

152 TYPE: Nucleic Acid

153 STRANDEDNESS: Double

154 TOPOLOGY: Linear

155 MOLECULE TYPE: TopoLibo

156 US 08 826 980 1

157 Query Match: 2.5% Score 19; PH 1; Length 2987;

158 Best Local Similarity: 10.0%; Prod. No. 16;

159 Matches: 19; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

160 267 atgaattgaataaaat 285

161 111111111111111111

162 1446 ATGATGAAATGAAACAC11 1463

OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,439  
FILING DATE:  
CLASSIFICATION: 510  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 03/424,641  
FILING DATE: April 19, 1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: Quest 4 1-155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5972674e  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2987 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
MOLECULE TYPE:  
US-08-826-439-1

Query Match 2.58; Score 19; DB 2; Length 2987;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 267 atgaattgataaagaatt 285  
|||||  
DB 1446 ATCAATTGATCAAGACTT 1464

RESULT 5  
US-08-913-159-1  
Sequence 1, Application US/08913159  
Patent No. 6300109  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Plasmid-derived type II  
TITLE OF INVENTION: restriction-modification systems from *Lactococcus lactis*  
NUMBER OF SEQUENCES: 14  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPD)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/913,159  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 0179/95  
FILING DATE: 17-FEB-1995  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3695 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: *Lactococcus lactis* subsp. *cremoris*  
STRAIN: W9  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 769..1620  
IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /codon\_start- 769  
OTHER INFORMATION: /product- "L1A1 -GATC- N-6-adenine methylase A"  
OTHER INFORMATION: /evidence- EXPERIMENTAL  
OTHER INFORMATION: /gene- "ORF"  
OTHER INFORMATION: /number- 1  
OTHER INFORMATION: /standard\_name- "Gene coding for M.L1A1A"  
OTHER INFORMATION: /label- m.l1a1a  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1613..2419  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /codon\_start- 1613  
OTHER INFORMATION: /product- "L1A1 GATC adenine methylase B"  
OTHER INFORMATION: /evidence- EXPERIMENTAL  
OTHER INFORMATION: /gene- "ORF"  
OTHER INFORMATION: /number- 2  
OTHER INFORMATION: /standard\_name- "Gene coding for M.L1A1B"  
OTHER INFORMATION: /label- m.l1a1b  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2412..3323  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /codon\_start- 2412  
OTHER INFORMATION: /product- "L1A1 restriction endonuclease"  
OTHER INFORMATION: /evidence- EXPERIMENTAL  
OTHER INFORMATION: /gene- "ORF"  
OTHER INFORMATION: /number- 3  
OTHER INFORMATION: /standard\_name- "Gene coding for L1A1 restriction  
OTHER INFORMATION: /label- r.l1a1

Query Match 2.68; Score 19; DB 4; Length 3695;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 267 atgaattgataaagaatt 285  
|||||  
DB 2118 ATCAATTGATCAAGACTT 2136

RESULT 6  
US-08-913-159-3  
Sequence 3, Application US/08913159  
Patent No. 6300109  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Plasmid-derived type II  
TITLE OF INVENTION: restriction modification systems from *Lactococcus lactis*  
NUMBER OF SEQUENCES: 14  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPD)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/913,159  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 0179/95  
FILING DATE: 17-FEB-1995  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3695 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: *Lactococcus lactis* subsp. *cremoris*



ADDRESSEE: Morrison & Foerster  
STREET: 545 Middlefield Road, Suite 200  
CITY: Menlo Park  
STATE: California  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/03680  
FILING DATE: 19910524  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 4610-0011.40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-327-7290  
TELEFAX: 415-327-2951  
TELEX: 706141  
INFORMATION FOR SEQ. ID NO: 156:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-JS91-03680-156

Query Match 2.5%; Score 18; DB 5; Length 25;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agagagaaagagagag 18  
|||||  
Db 5 AGAGAGAAAAGAGAGAG 22

RESULT 10  
US-08-378-588-15  
Sequence 15, Application US/08378588  
Patent No. 5608148  
GENERAL INFORMATION:  
APPLICANT: John, Maliyakal E.  
TITLE OF INVENTION: TRANSGENIC COTTON PLANTS  
TITLE OF INVENTION: PRODUCING HETEROLOGOUS PEROXIDASE  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nicholas J. Seay, Quarles & Brady  
STREET: First Wisconsin Plaza, One South  
STREET: Pinckney St.,  
STREET: P.O. Box 2113  
CITY: Madison  
STATE: WI  
COUNTRY: USA  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,588  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
REFERENCE/DOCKET NUMBER: 11-229-9101 2  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-2484  
TELEFAX: (608) 251-9166  
INFORMATION FOR SEQ. ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1064 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-378-588-15

Query Match 2.5%; Score 18; DB 1; Length 1064;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 699 taattaattaataatca 716  
|||||  
Nb 785 TAATTAATTAATTAATCA 802

RESULT 11  
US-08-811-094-15  
Sequence 15, Application US/08811094  
Patent No. 5869720  
GENERAL INFORMATION:  
APPLICANT: John, Maliyakal E.  
TITLE OF INVENTION: TRANSGENIC COTTON PLANTS  
TITLE OF INVENTION: PRODUCING HETEROLOGOUS PEROXIDASE  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nicholas J. Seay, Quarles & Brady  
STREET: First Wisconsin Plaza, One South  
STREET: Pinckney St.,  
STREET: P.O. Box 2113  
CITY: Madison  
STATE: WI  
COUNTRY: USA  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/811,094  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/378,588  
FILING DATE: 25-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
REFERENCE/DOCKET NUMBER: 11-229-9101-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 251-2484  
TELEFAX: (608) 251-9166  
INFORMATION FOR SEQ. ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1064 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-811-094-15

Query Match 2.5%; Score 18; DB 2; Length 1064;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 699 taattaattaataatca 716



Job time: 8.235 sec

INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1270 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-811-094-23

Query Match 2.5%: Score 18; DB 2; Length 1270;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 699 taattaataataatca 716  
 ||||||||||||||||  
 Db 991 TAATTAATTAATTAATCA 1008

RESULT 15  
 PCT-US94-11121-23  
 Sequence 23. Application PC/TUS9411121  
 GENERAL INFORMATION:  
 APPLICANT: John, Mallyakal E.  
 TITLE OF INVENTION: TRANSGENIC COTTON PLANTS  
 TITLE OF INVENTION: PRODUCING HYPERLOGOUS PEROXIDASE  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nicholas J. Seay, Charles & Brady  
 STREET: First Wisconsin Plaza, One South  
 STREET: Pinckney St.  
 STREET: P.O. Box 2113  
 CITY: Madison  
 STATE: WI  
 COUNTRY: USA  
 ZIP: 53701-2113  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/11121  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seay, Nicholas J.  
 REGISTRATION NUMBER: 27,386  
 REFERENCE/DOCKET NUMBER: 11-229-9076-8  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (608) 251-2484  
 TELEFAX: (608) 251-9166  
 INFORMATION FOR SEQ ID NO: 23:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1270 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 PCT-US94-11121-23

Query Match 2.5%: Score 18; DB 5; Length 1270;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 699 taattaataataatca 716  
 ||||||||||||||||  
 Db 991 TAATTAATTAATTAATCA 1008

Search completed: September 1, 2002, 03:12:46

